

FIG. 1A

FIG. 1B-1

TGG AAC TTC CTG GAA TCC TTT TAT TTT TGT TTT ATT TCC CTG AGC ACC ATT GGC CTG W N F L E S F Y F C F I S L S T I G L	684 228
GGG GAT TAT GTG CCT GGG GAA GGC TAC AAT CAA AAA TTC AGA GAG CTC TAT AAG ATT G D Y V P G E G Y N Q K F R E L Y K I	741 247
GGG ATC ACG TGT TAC CTG CTA CTT GGC CTT ATT GCC ATG TTG GTA GTT CTG GAA ACC G I T C Y L L G L I A M L V V L E T	798 266
TTC TGT GAA CTC CAT GAG CTG AAA AAA TTC AGA AAA ATG TTC TAT GTG AAG AAG GAC F C E L H E L K K F R K M F Y V K K D	855 285
AAG GAC GAG GAT CAG GTG CAC ATC ATA GAG CAT GAC CAA CTG TCC TTC TCC TCG ATC K D E D Q V H I I E H D Q L S F S S I	912 304
ACA GAC CAG GCA GCT GGC ATG AAA GAG GAC CAG AAG CAA AAT GAG CCT TTT GTG GCC T D Q A A G M K E D Q K Q N E P F V A	969 323
ACC CAG TCA TCT GCC TGC GTG GAT GGC CCT GCA AAC CAT TGA gcgttaggattttgcatt T Q S S A C V D G P A N H *	1030 337
atgctagagcaccagggtcagggtcaaggaagaggcttaagtatgttcattttatcagaatgcggaaaaaa ttatgtcacttaagaaatagctactgtttcaatgtcttattaaaaacaacaaaaagacacatggAACAG aagctgtgaccccgaggatgtctaataatgtgagaaatgagatgtccaccaaattcatatgtgacaaaatta tctcgaccttacataggaggagaataacttgaaggcagtatgctgtggtagaaggcagattttatacttttaact ggaaactttgggtttgcatttagatcatttagctgatggctaaatgcaaaatttatattagaagcaaaaaaaa aaagcatagagatgtttataaatagtttatgttactggttgcattgtacccacccaaaatgatttttg gagaatctaagtcaaactcactattataatgcataggtaaccattaaactatgtacatataaagtataatgtt tatattctgtacatatggtttaggtcaccagatccttagtgttagttctgaaactaagactataatgttatttt ttttagttctttataactaaagaatccagatgtgcataaaaataagggaataataaaaaaaaaaaaaaa	1106 1182 1258 1334 1410 1486 1562 1638 1712

FIG. 1B-2

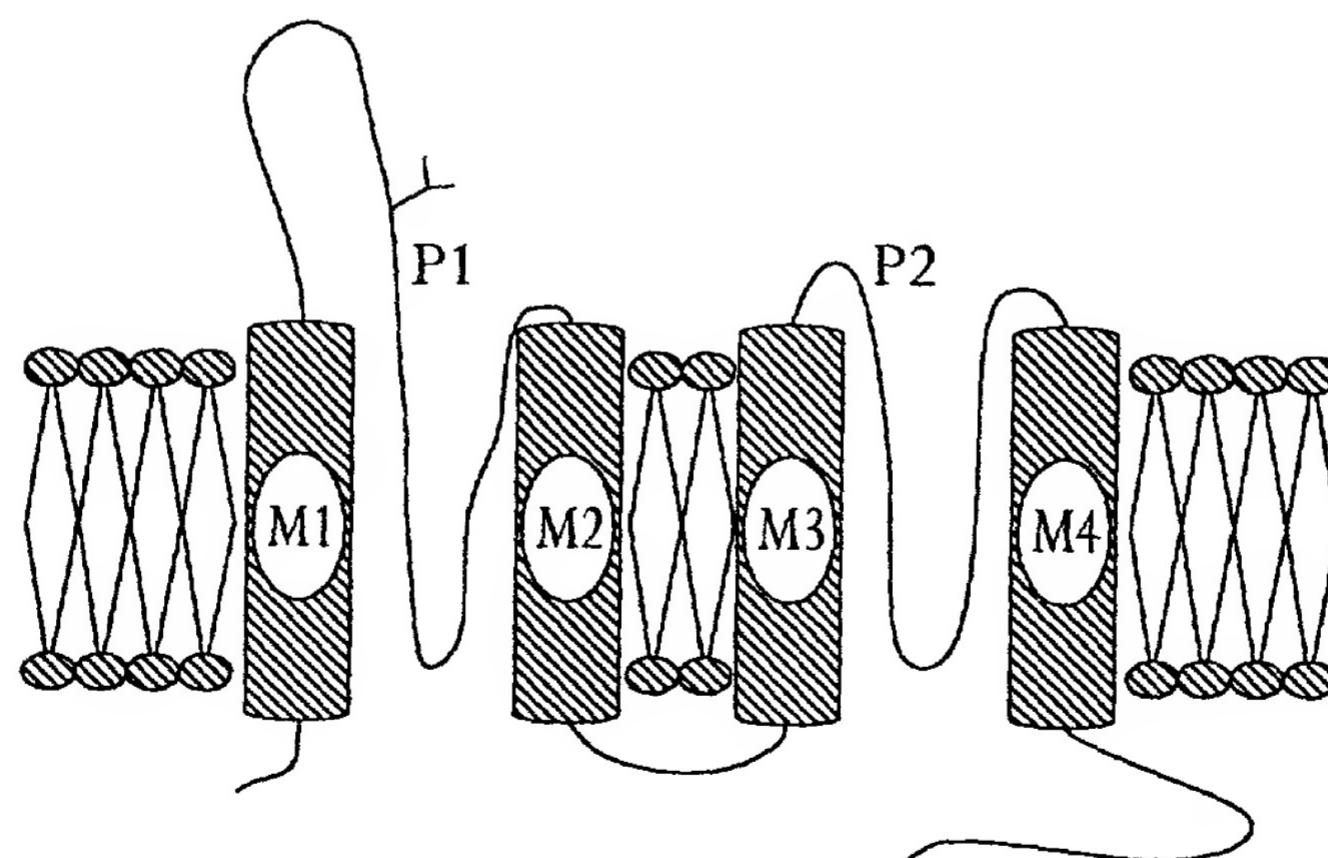
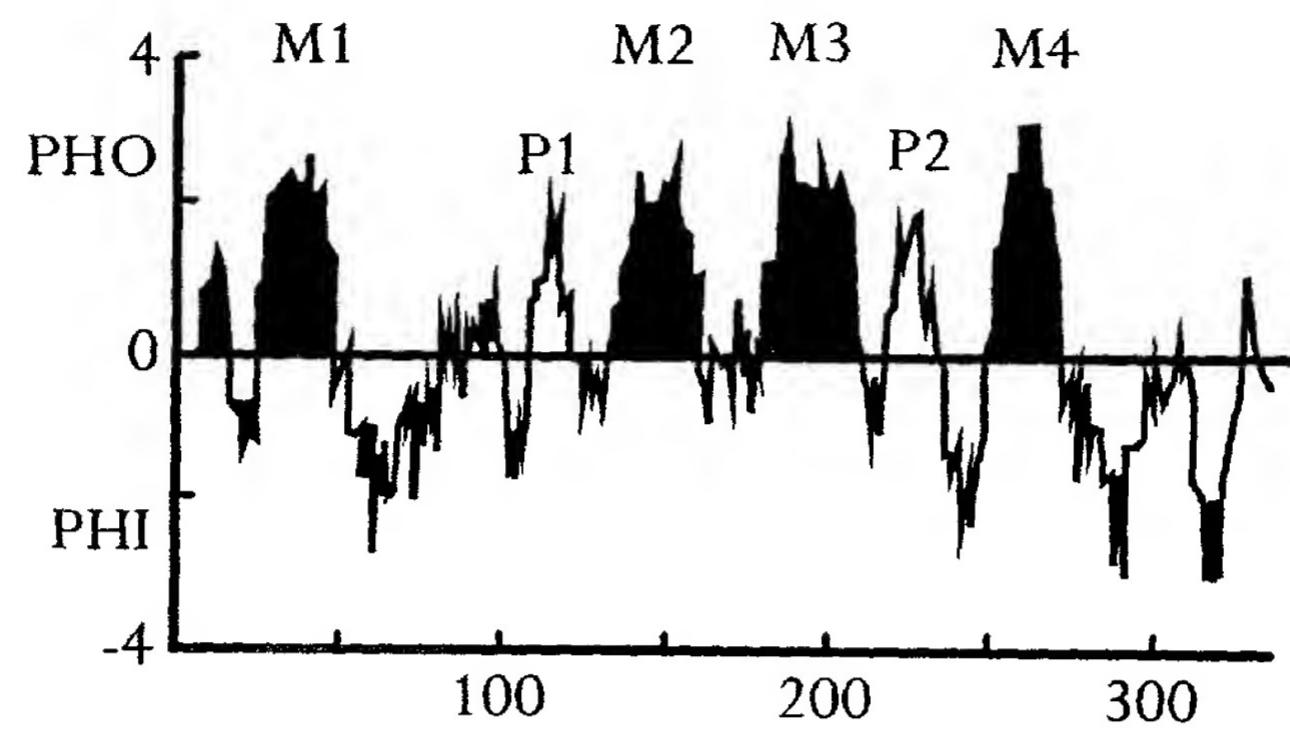


FIG. 1C

	1	14	27
TWIK-1 P1	F T S A L E F A S T V I S T T G Y G H T V P L S D G C		
TWIK-1 P2	E L E S F Y E C F I S L S T I C L G D Y V P G E G Y N		
TOK1 P2	Y F N C I Y E C F I C L L T I G Y G D Y A P R T G A Q		
TOK1 P1	Y G N A L Y F C T V S L L T V G L G D I L P K S V G A		
Slo	Y W T C V Y F L I V T M S T V G Y G D V Y C E T V L G		
Shaker	I P D A F W W A V V T M T T V G Y G D M T P V G F W G		
Shab	I P E A F W W A G I T M T T V G Y G D I C P T T A L G		
Shal	I P A A F W Y T I V T M T T L G Y G D M V P E T I A G		
Shaw	I P I G I W W A I V T M T T V G Y G D M A R K T Y I G		
KAT1	Y V T A L Y W S I T T L T T I G Y G D F H A E N P R E		
AKT1	Y V T S M Y W S I T T L T T V G Y G D I H P V N T K E		
eag	Y V T A L Y E T M T C M T S V G E G N V A A E T D N E		
ROMK1	M T S A F L E S L E T Q V T I G Y G F R F V T E Q C A		
IRK1	F T A A E L E S I E T Q T T I G Y G F R C V T D E C P		
GIRK1	F P S A F L E F I E T E A T I G Y G Y R Y I T D K C P		

FIG. 2A

TWIK-1	1	MLQSLAGSSCVREVE-----RHRSAWCF--GE-----LVLGY
f17c8	1	MYTDEGEYSGDTDHGGSTIMOKMSPNTRONFRQNVVVCLSAATI-----
M110-2	1	MTVSMEENSKEQMSATSKDVKVATDR\$LLNKYHLGPLEALITGLVESC
TWIK-1	31	L EYLVF GAVV ESS VELPYEELLROE-----LRKLKRRE EE H C ---L
f17c8	47	L VENLIGAG E-----YAE T ONS S ES
M110-2	49	V TYALGGAY EL SIEHP EELKRREKAIREFQDLKQOEMCNITSGIEN
TWIK-1	71	SEODOLEOELGR VE -----EAENYGVSV D SNASGNWNW-----DFT S ALF
f17c8	69	L NENSEV --SKCLHNLPIGGKITAEMKS KLGK CTKSSRIDGE GKA I
M110-2	96	SEOS EE EYTKK E LMLED AHNAH AFFYFFLNHEIPKDMW-----TESSAIV
P1		
TWIK-1	110	FAS T V EST T GYGHTV P E S DGGKAFC II -Y S VIGT P FT L LE F ITAVVORI
f17c8	115	FSW TE Y ST V GYG S I X PH S T L GR Y ET I F-Y S LJMD P V F IAFKFEFG T
M110-2	142	FT TTTV I PV G Y G Y I E P V S A Y GR-M C L T A Y AL G I P FT L VT M AD G KA
TWIK-1	157	TV H---V TR RP V L-----Y E HERW G E S KOV V AT V H A V L L G E V TV S C F
f17c8	162	A H FLVV V V S N R T R AVKKAY K S -Q N P E NA E T P S N S L OH D Y I FL S SI
M110-2	189	A Q L---V T R-----W E G D NN M A I PAA F V-----C L I
P2		
TWIK-1	197	F I -PAAVFS--- VL --E DD DN E LES F K CF I S E ST I G L G D V R G E G Y N
f17c8	209	LL C S E G I L SS S AI F S I ENT S Y L S S V Y E G I T M F L I G G D V PT N ---
M110-2	213	FAYPL V VG F --- L C S TS N I T Y L S V Y F \$ L T\$ E FT I G G D I T P ---
TWIK-1	239	QKFRE EY K G E C Y E EL G L I A M V V I E T F C-----E E H L K K R-----
f17c8	254	-----L W F S G Y C M L F L I S D V I S N O I F Y FC Q A R V R Y F F H I L A R K I
M110-2	253	-----D M N V I H M V L F I A V G Y I L V T I L D VA---A E M I D R V H Y M G R H V G
TWIK-1	278	-----K M E Y V K K D K D D Q V H I E H D O L -----S F S E I T D O A A G M K E D
f17c8	295	LL R E-E DD G F O E L T T V S L O H E P I N S Q C M P S I-----V W D C E K E I D N D
M110-2	294	KAKELAGKMFO A Q S I N M K Q G L V SGVGQLHALARFGMLVGREEVDK Q
TWIK-1	315	Q K Q N E P F V A T -----Q S SAC V D G P A N H ---
f17c8	338	E K L I S S L E T S -----
M110-2	342	EDG I I A F S P D V M D G L E F M D T L S I Y S R R \$ RR S A E N S A R N L FL S

FIG. 2B

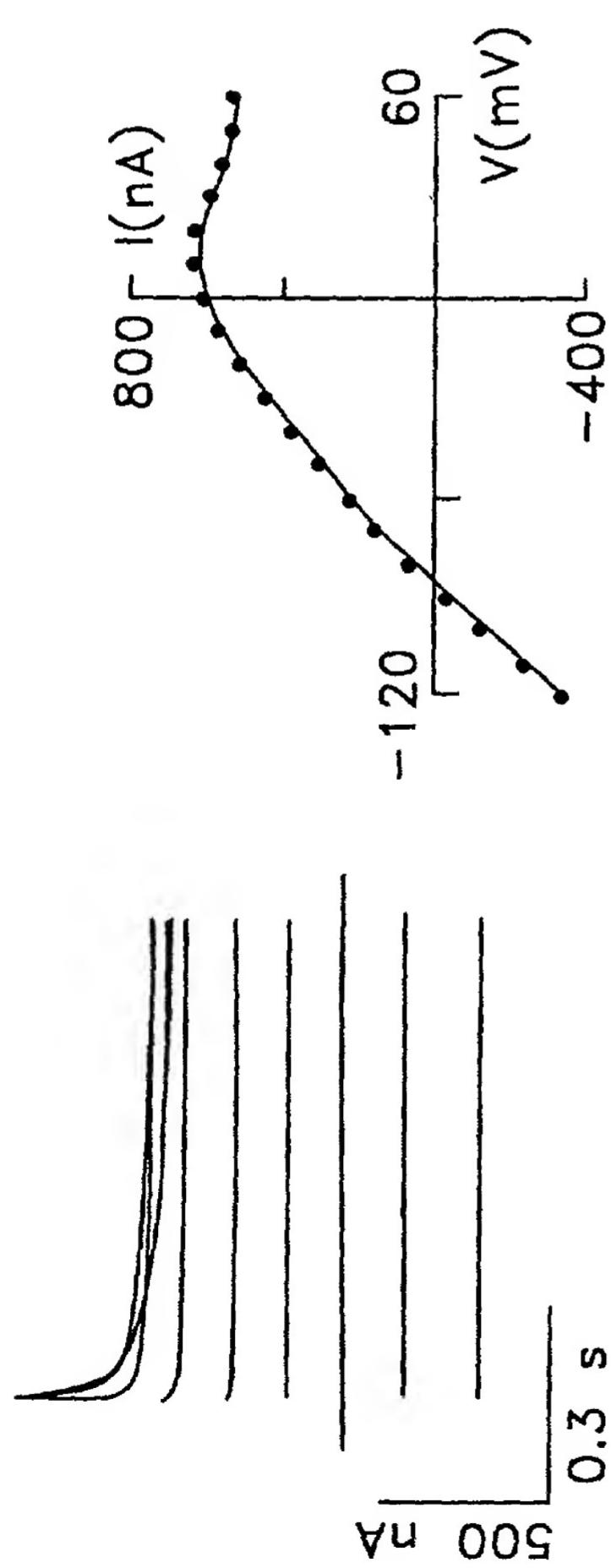


FIG. 3A

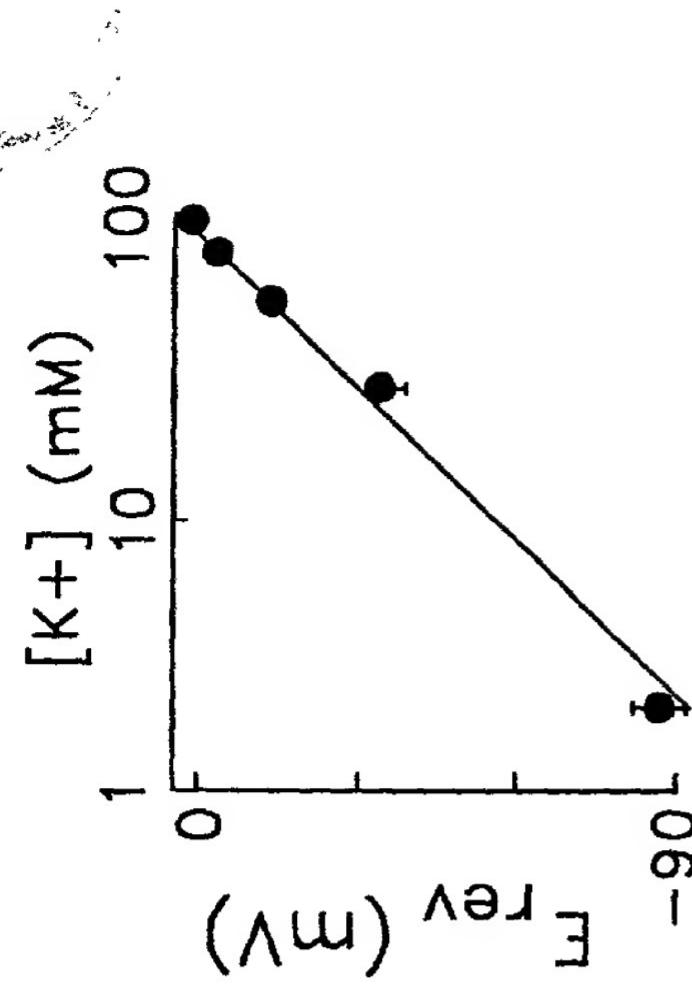


FIG. 3B

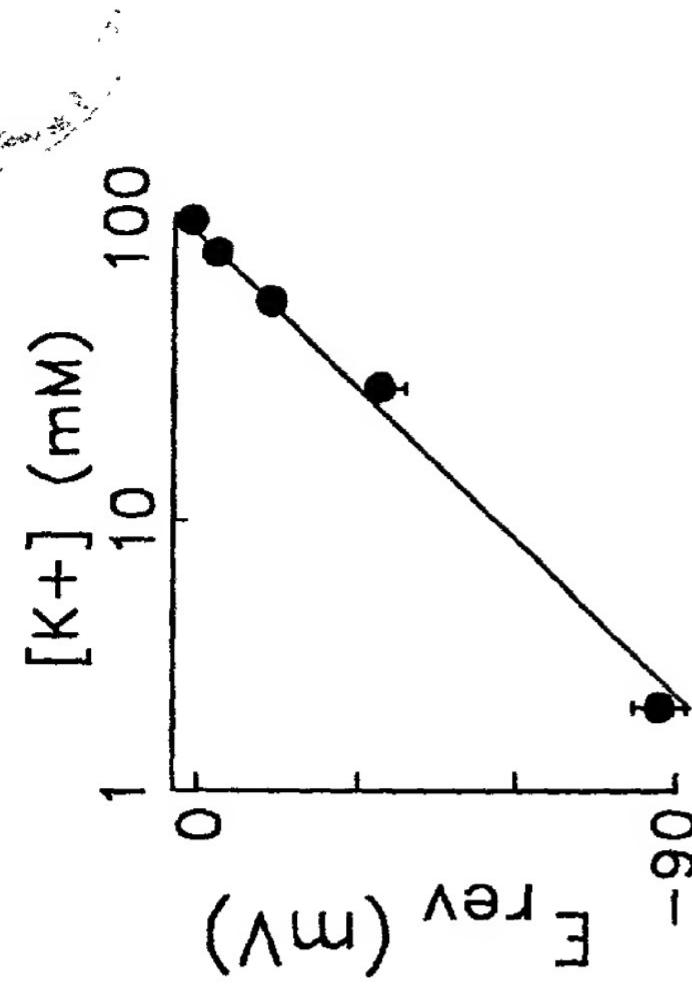


FIG. 3C

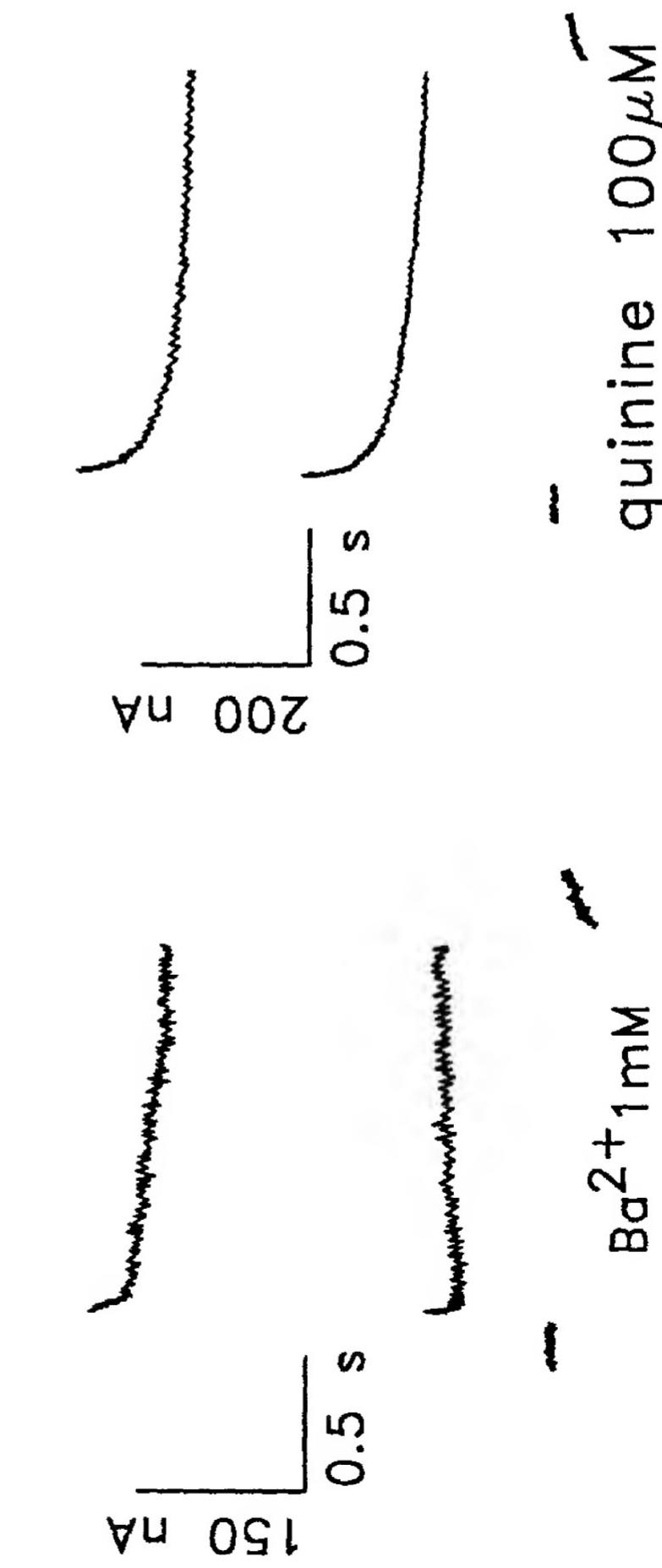


FIG. 3D

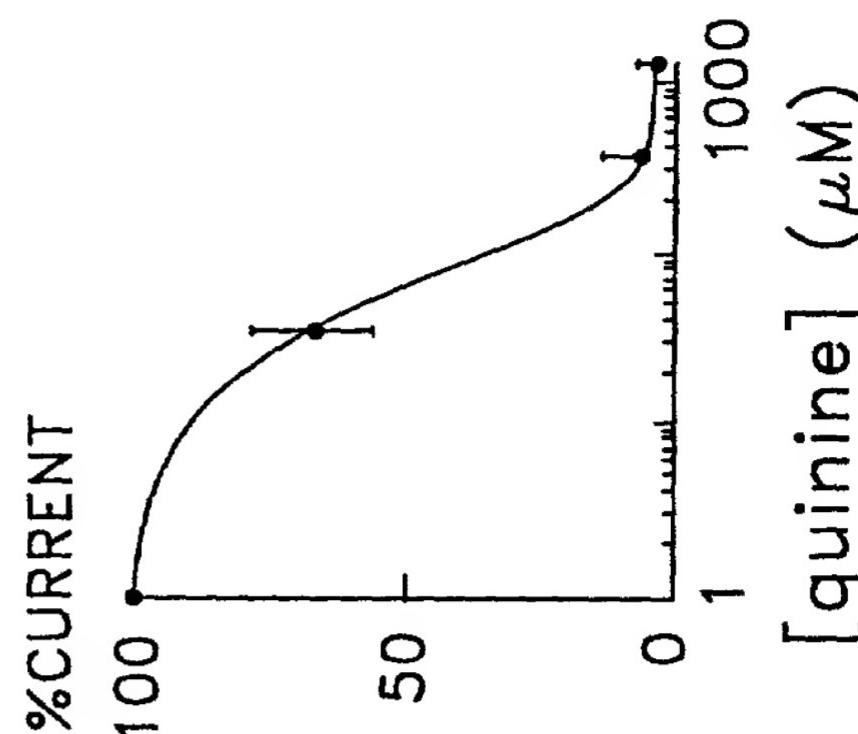


FIG. 3E

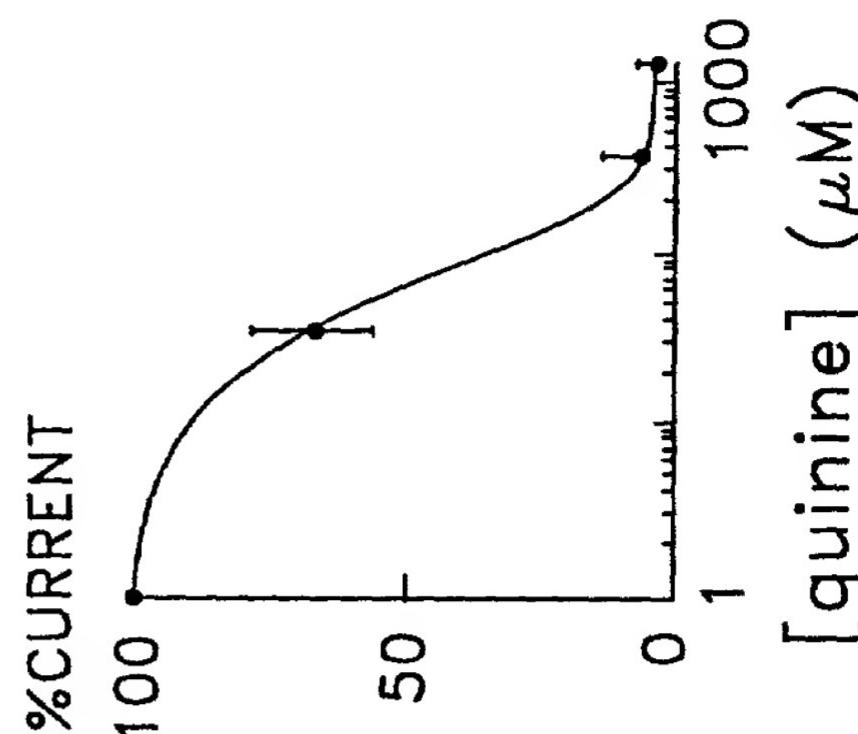


FIG. 3F

FIG. 4A

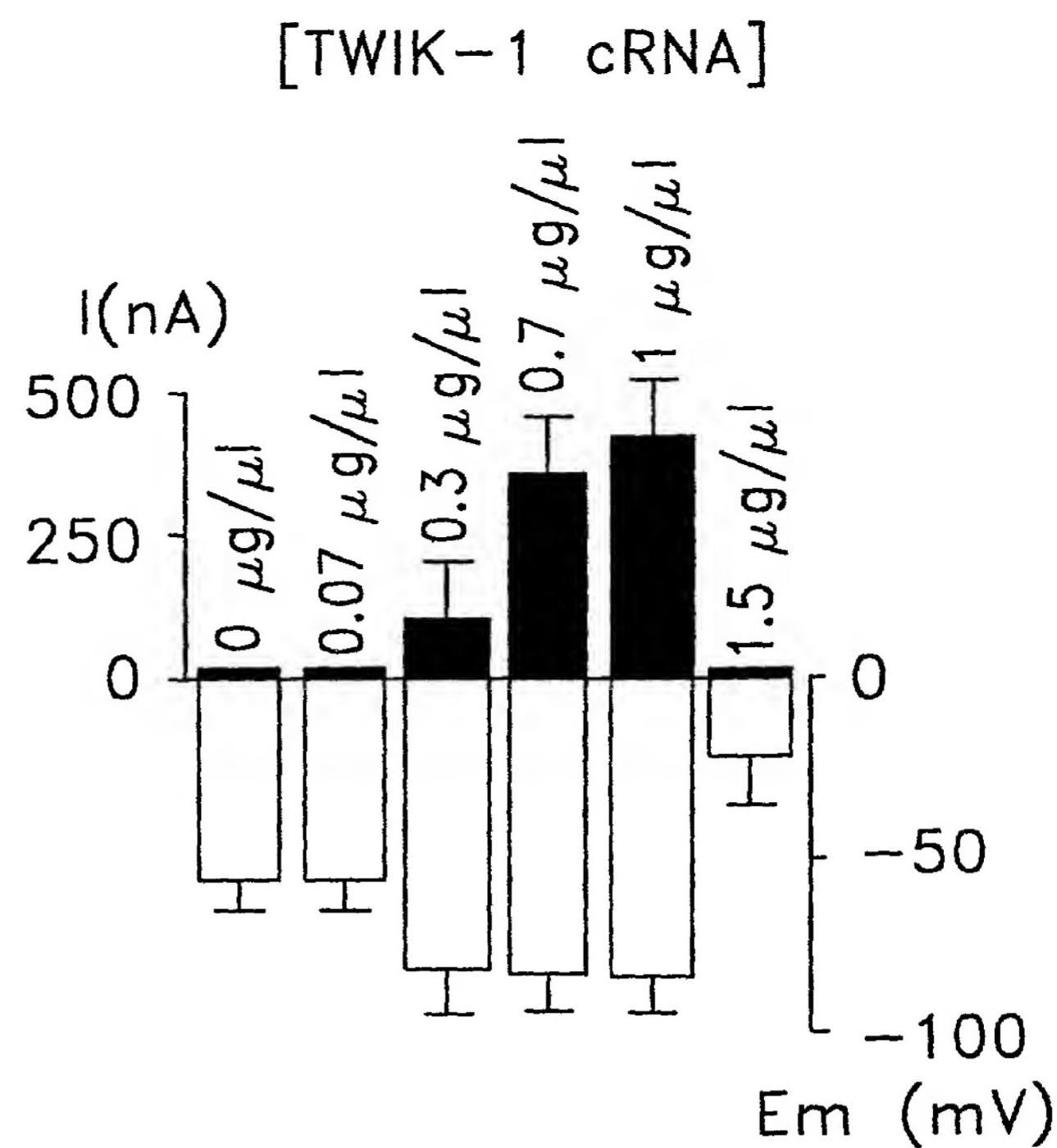


FIG. 4B

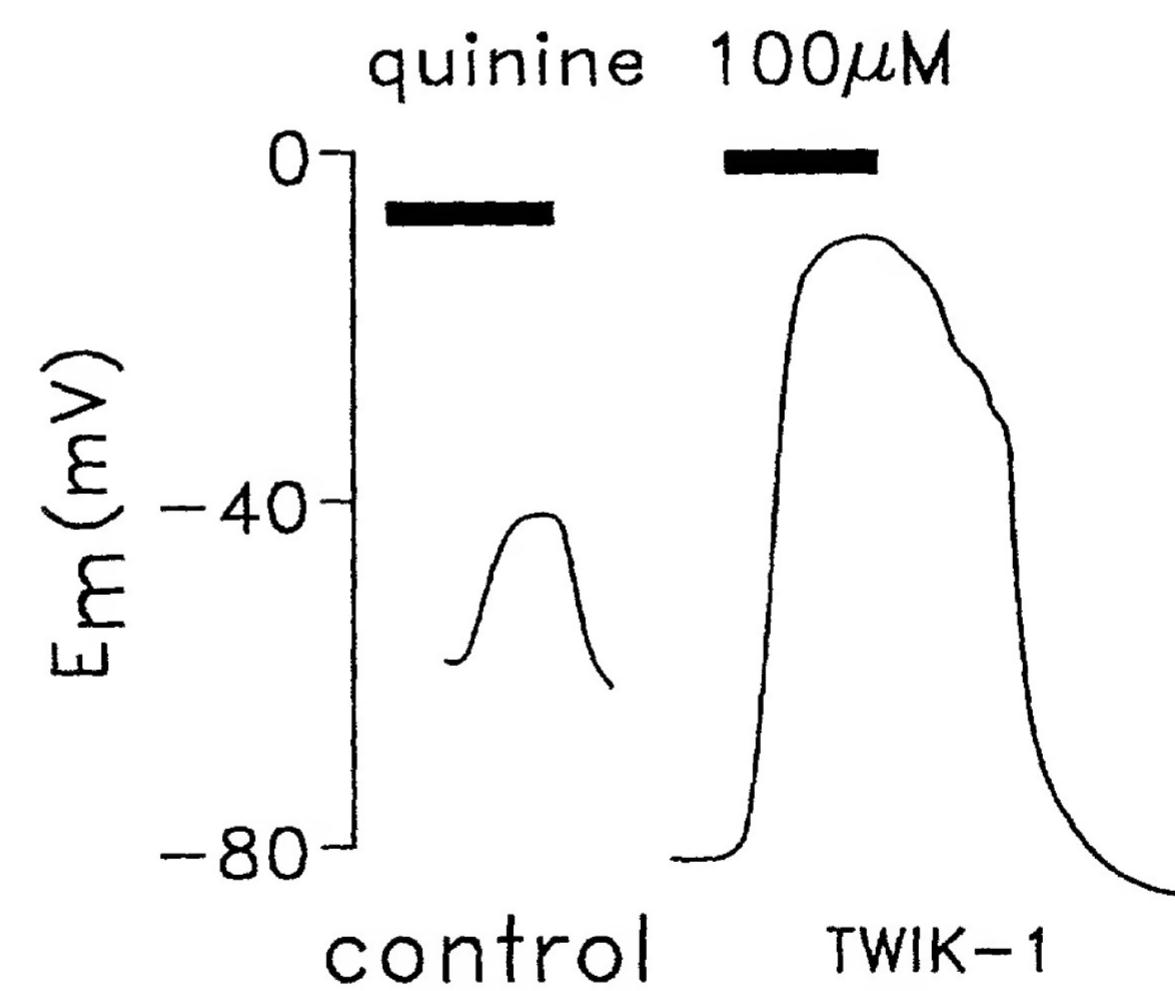
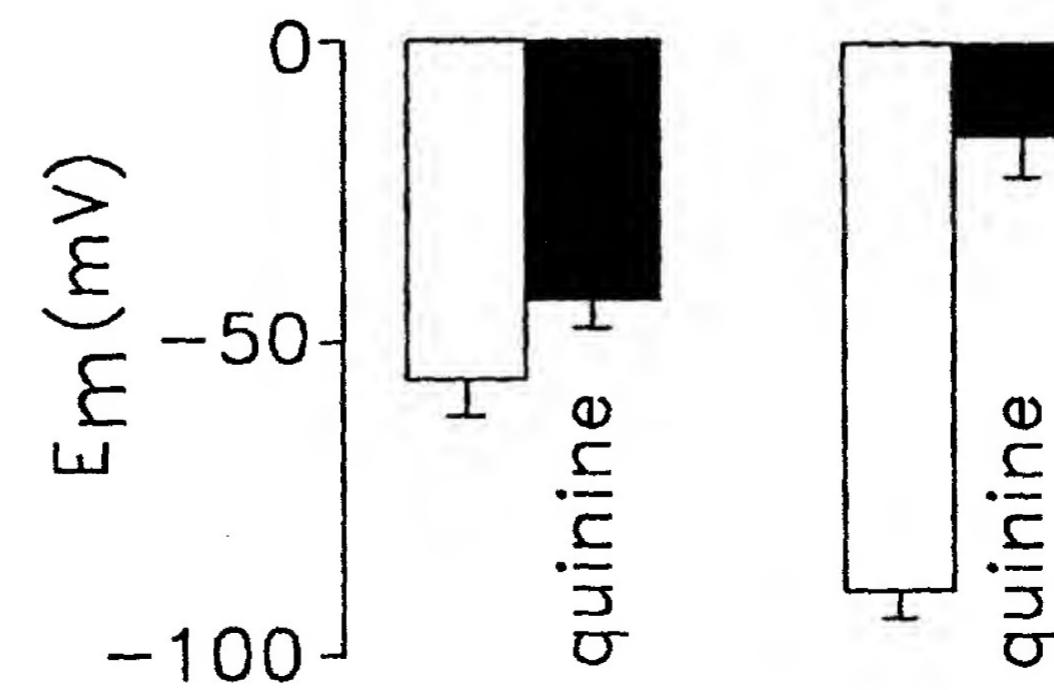


FIG. 4C



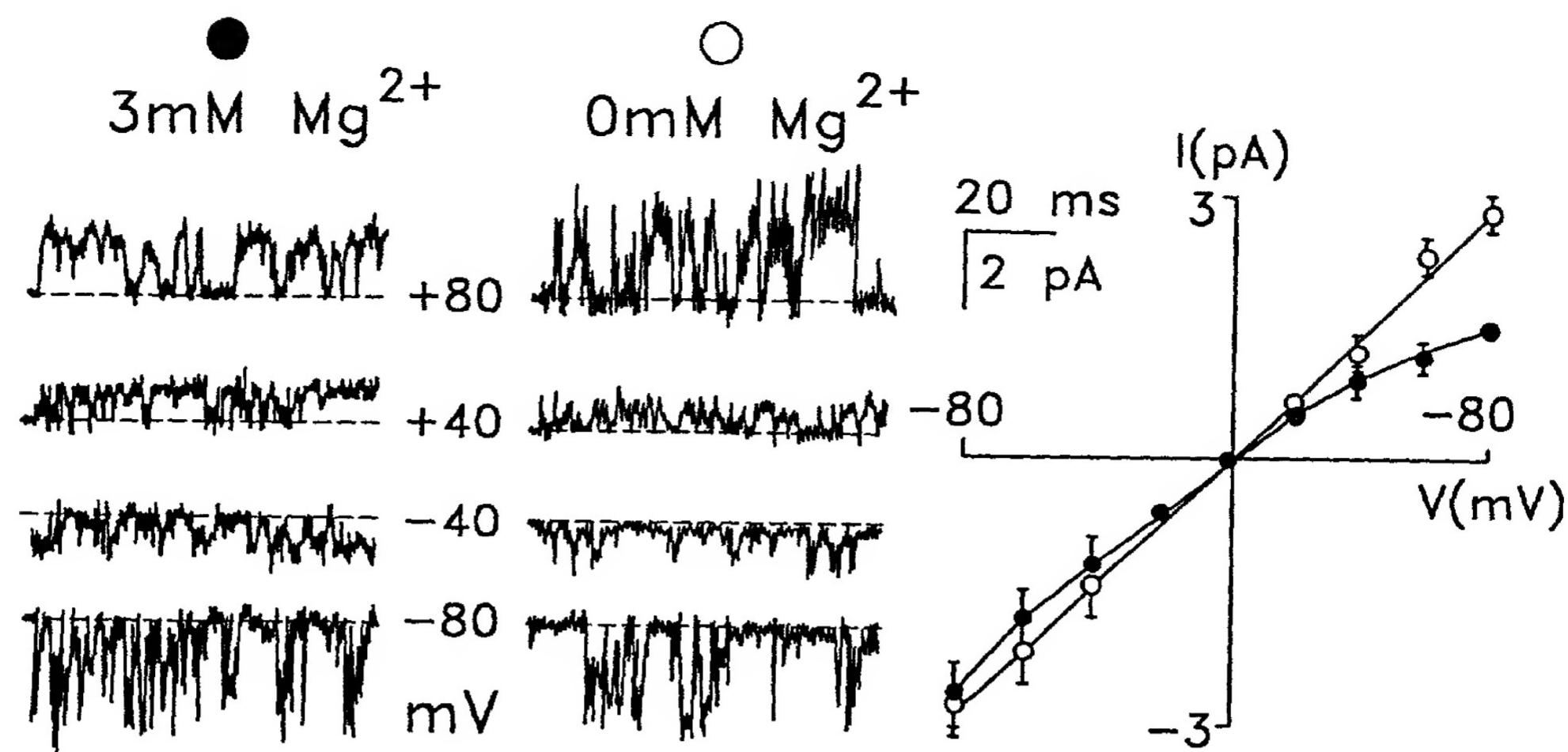


FIG. 5A

FIG. 5B

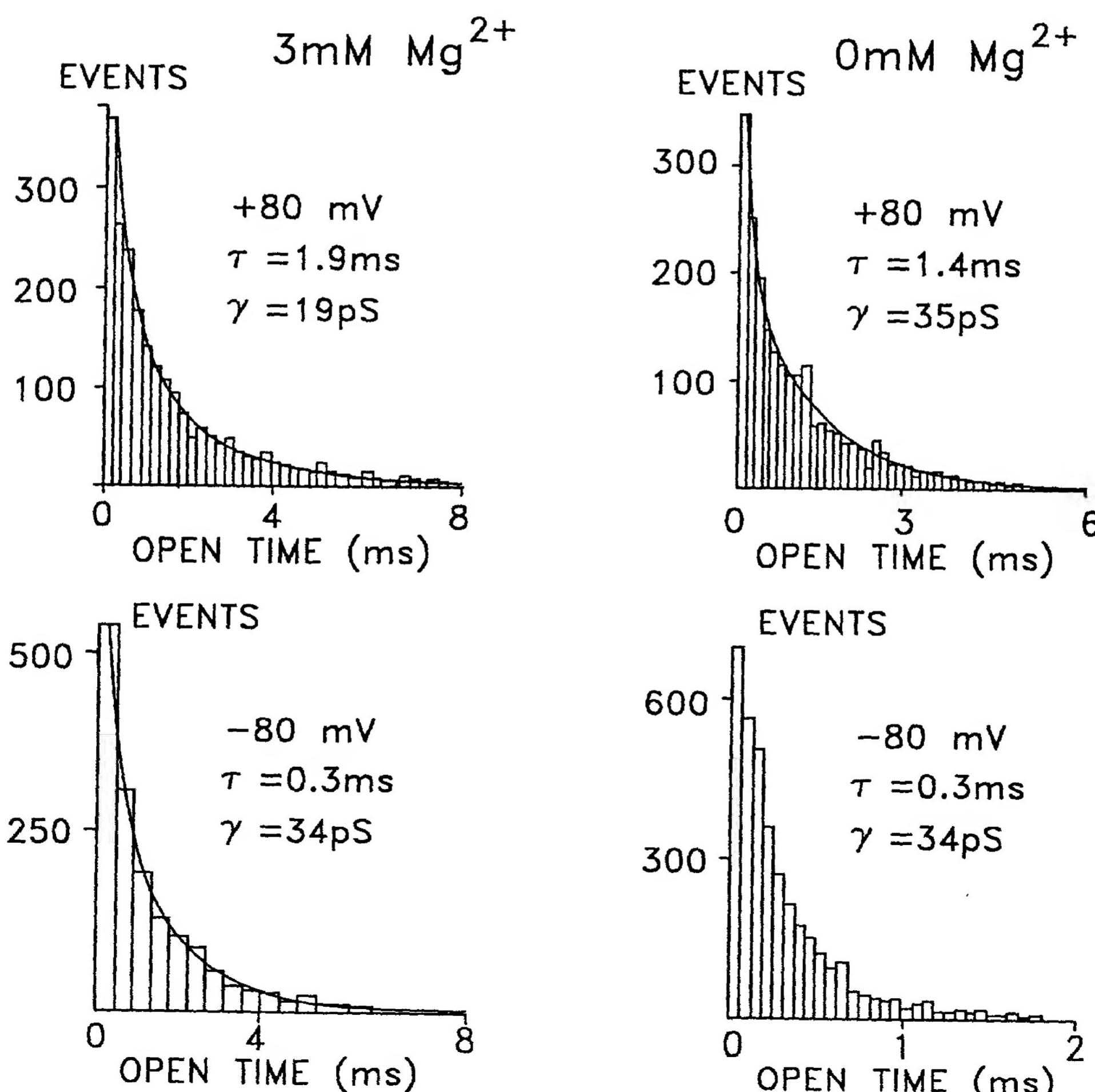


FIG. 5C

FIG. 5D

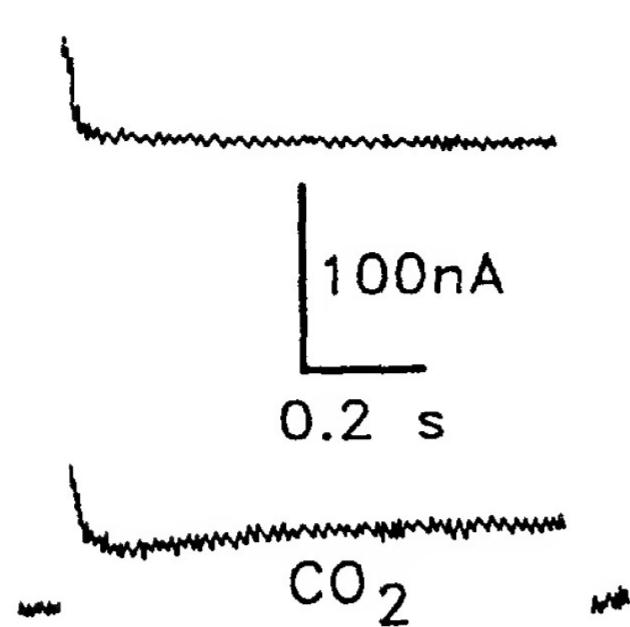


FIG. 6A

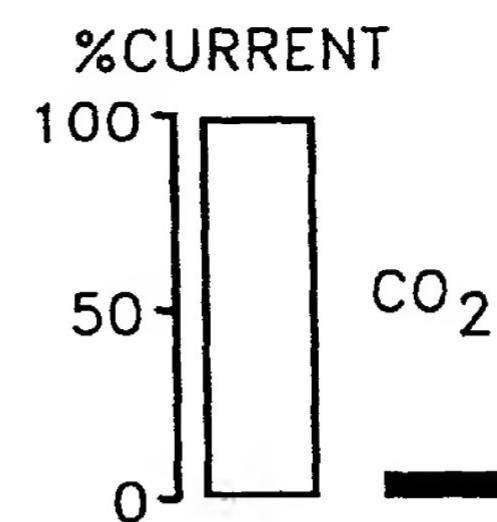


FIG. 6B

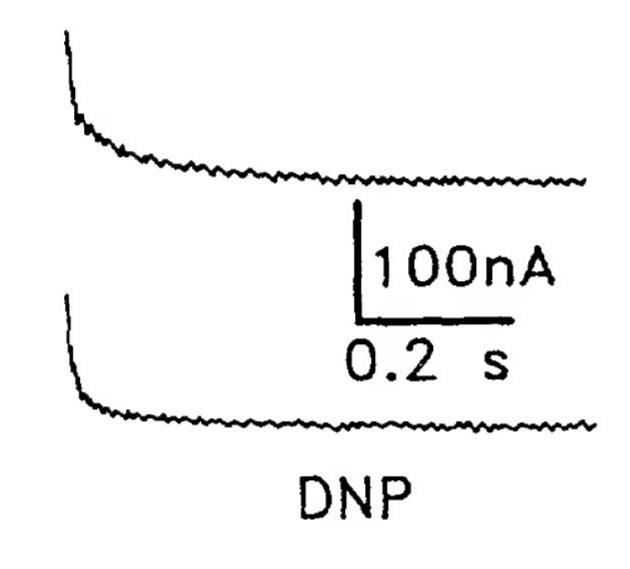


FIG. 6C

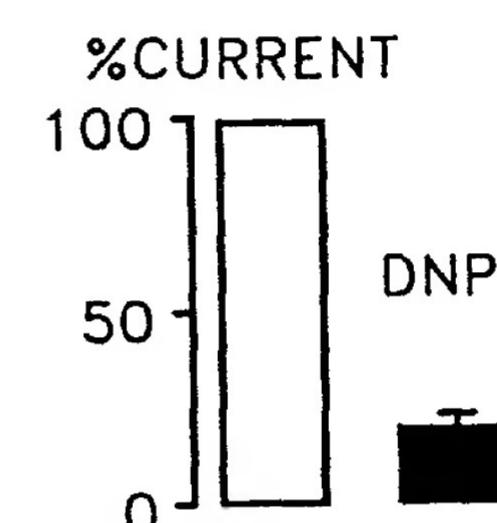


FIG. 6D

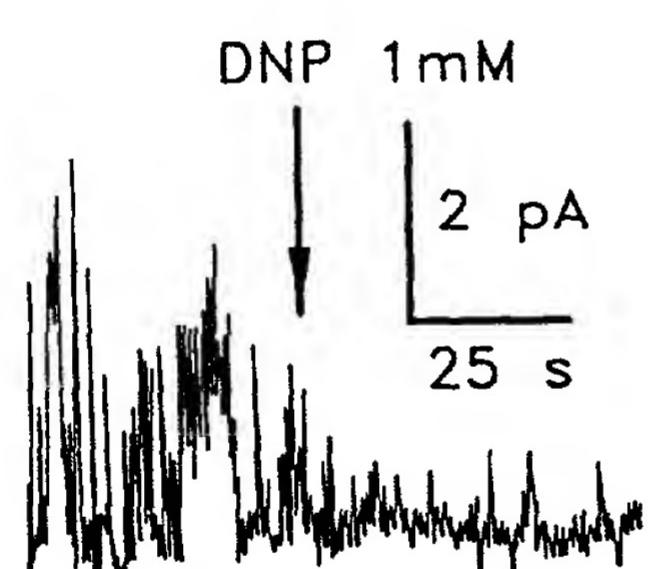


FIG. 6E

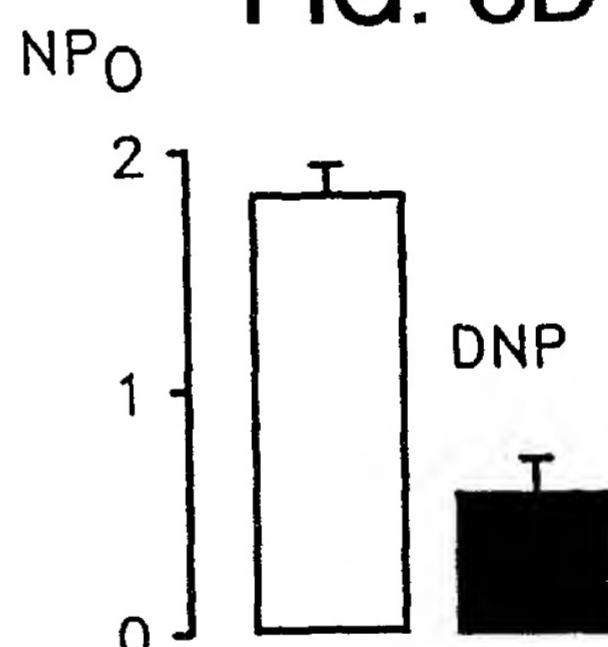


FIG. 6F

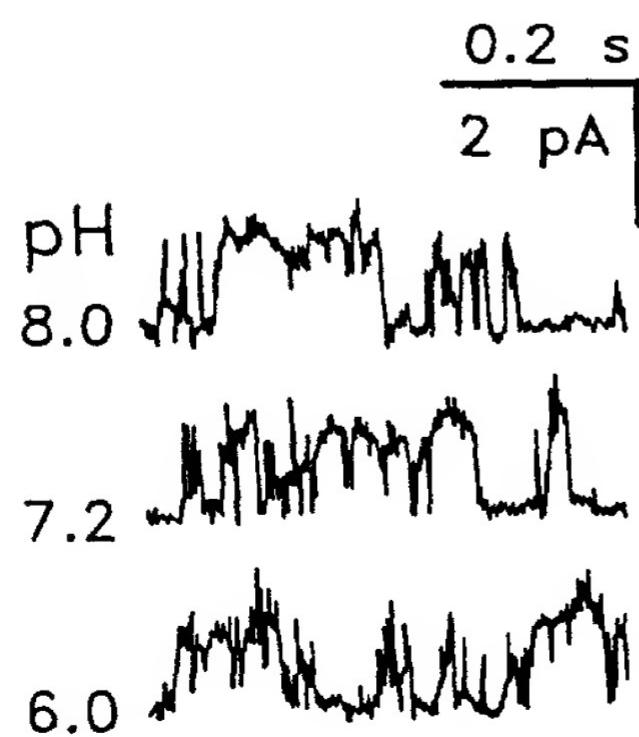


FIG. 6G

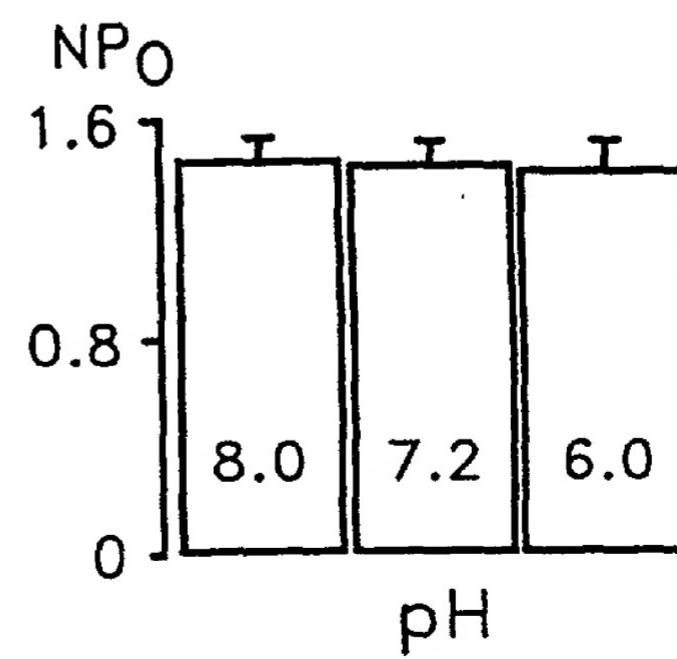


FIG. 6H

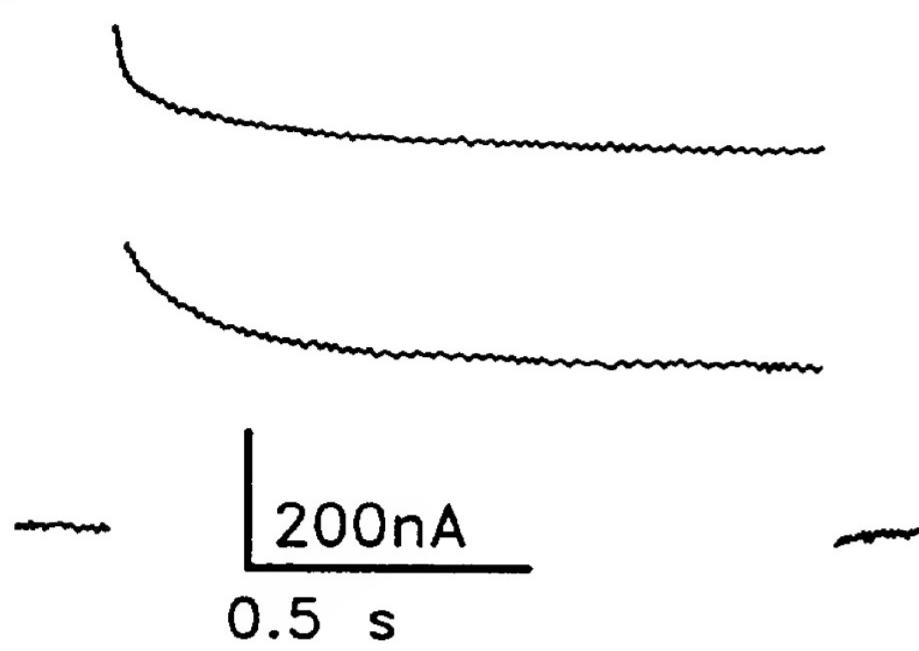


FIG. 7A

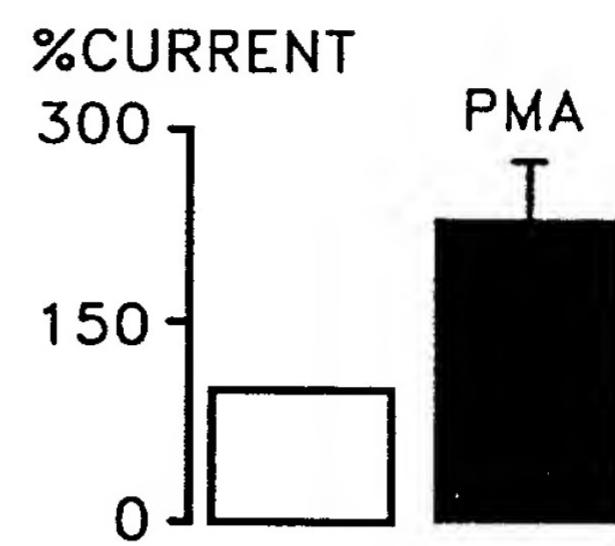


FIG. 7B

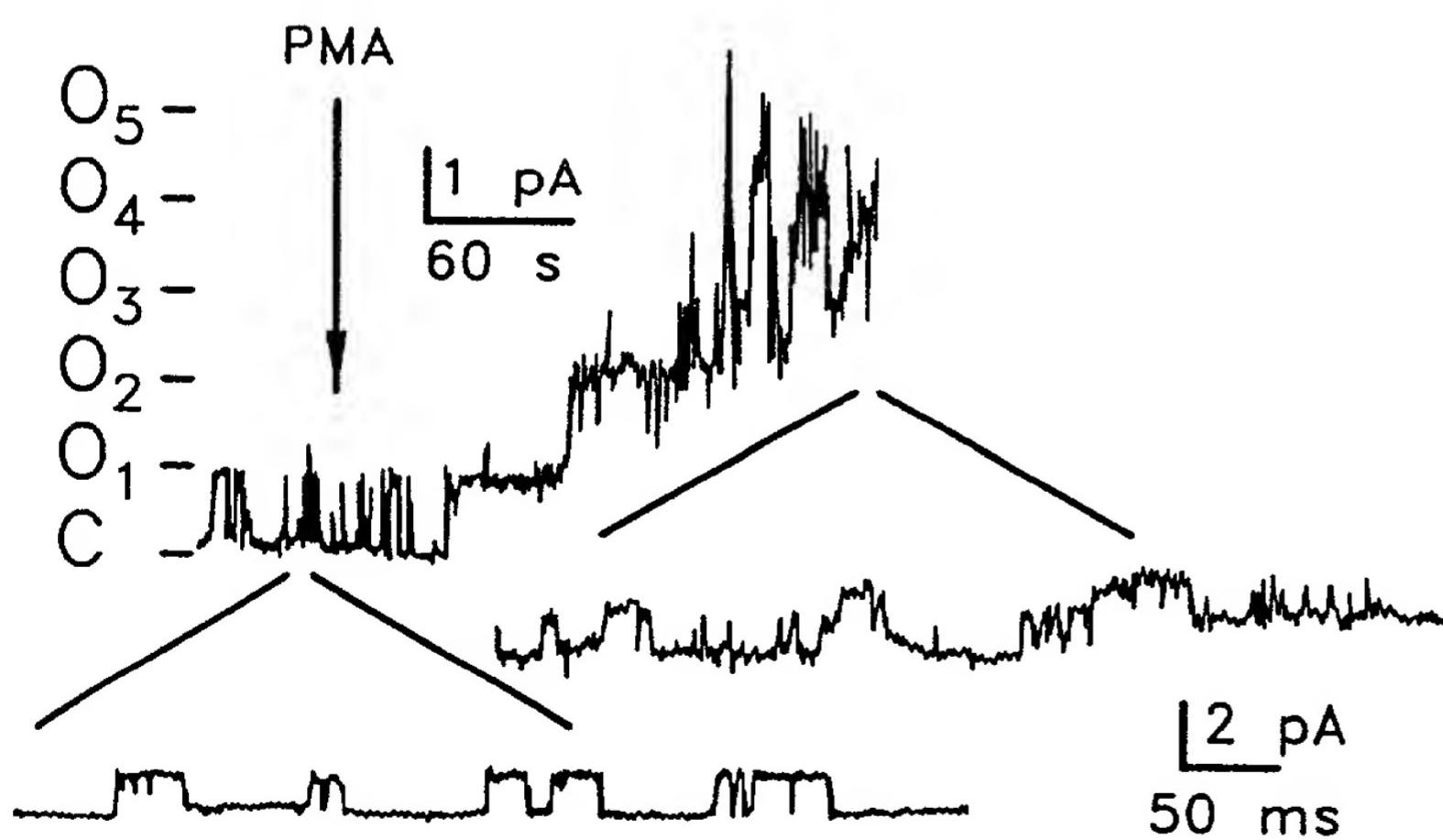


FIG. 7C

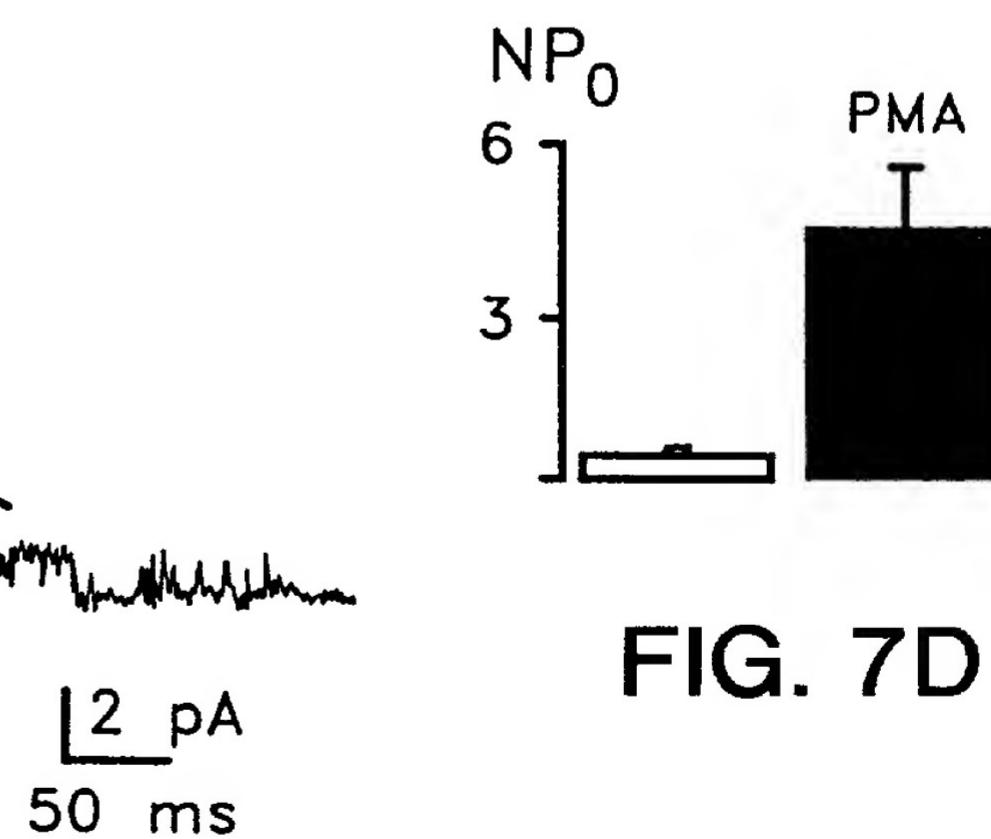


FIG. 7D

tgccctgcgcggatagcggcgagcgcagccatgccccaggccgcctccg -77
 gggcagcagcagcggcggccggggccatgcgcggggccggggccggccggccggacg -1

ATG	AAG	CGG	CAG	AAC	GTG	CGC	ACG	CTG	GCG	CTC	ATC	GTG	TGC	ACC	TTC	ACC	ACC	TAC	CTG	57
M	K	R	Q	N	V	R	T	L	A	L	I	V	C	T	F	T	Y	L	19	
	E	N	V	R	T	L	A	L	I	V	C	T	F	T	Y	L				
CTG	GTG	GGC	GCC	GCG	GTC	TTC	GAC	GCG	CTG	GAG	TCG	GAG	CCC	GAG	CTG	ATC	GAG	CGG	114	
L	V	G	A	A	V	F	D	A	L	E	S	E	P	E	L	I	E	R	38	
L	V	G	A	A	V	F	D	A	L	E	S	E	P	E	M	I	E	R		
CAG	CGG	CTG	GAG	CTG	CGG	CAG	CAG	GAG	CTG	CGG	GCG	CGC	TAC	AAC	CTC	AGC	CAG	GGC	171	
Q	R	L	E	L	R	Q	Q	E	L	R	A	R	Y	N	L	S	Q	G	57	
Q	R	L	E	L	R	Q	L	E	L	R	A	R	Y	N	L	S	E	G		
*																				
GGC	TAC	GAG	GAG	CTG	GAG	CGC	GTC	GTG	CTG	CGC	CTC	AAG	CCG	CAC	AAG	GCC	GGC	GTG	228	
G	Y	E	E	L	E	R	V	V	L	R	L	K	P	H	K	A	G	V	76	
G	Y	E	E	L	E	R	V	V	L	R	L	K	P	H	K	A	G	V		
CAG	TGG	CGC	TTC	GCC	GGC	TCC	TTC	TAC	TTC	GCC	ATC	ACC	GTC	ATC	ACC	ACC	ATC	GGC	285	
Q	W	R	F	A	G	S	F	Y	F	A	I	T	V	I	T	T	I	G	95	
Q	W	R	F	A	G	S	F	Y	F	A	I	T	V	I	T	T	I	G		
TAC	GGG	CAC	GCG	GCA	CCC	AGC	ACG	GAT	GGC	GGC	AAG	GTG	TTC	TGC	ATG	TTC	TAC	GCG	342	
Y	G	H	A	A	P	S	T	D	G	G	K	V	F	C	M	F	Y	A	114	
Y	G	H	A	A	P	S	T	D	G	G	K	V	F	C	M	F	Y	A		
CTG	CTG	GGC	ATC	CCG	CTC	ACG	CTC	GTC	ATG	TTC	CAG	AGC	CTG	GGC	GAG	CGC	ATC	AAC	399	
L	L	G	I	P	L	T	L	V	M	F	Q	S	L	G	E	R	I	N	133	
L	L	G	I	P	L	T	L	I	M	F	Q	S	L	G	E	R	I	N		
ACC	TTG	GTG	AGG	TAC	CTG	CTG	CAC	CGC	GCC	AAG	AAG	GGG	CTG	GGC	ATG	CGG	CGC	GCC	456	
T	L	V	R	Y	L	L	H	R	A	K	K	G	L	G	M	R	R	A	152	
T	E	V	R	Y	L	L	H	R	A	K	R	G	L	G	M	R	H	A		
GAC	GTG	TCC	ATG	GCC	AAC	ATG	GTG	CTC	ATC	GGC	TTC	TTC	TCG	TGC	ATC	AGC	ACG	CTG	513	
D	V	S	M	A	N	M	V	L	I	G	F	F	S	C	I	S	T	L	171	
E	V	S	M	A	N	M	V	L	I	G	F	V	S	C	I	S	T	L		
TGC	ATC	GGC	GCC	GCC	TTC	TCC	CAC	TAC	GAG	CAC	TGG	ACC	TTC	TTC	CAG	GCC	TAC	570		
C	I	G	A	A	A	F	S	H	Y	E	H	W	T	F	F	Q	A	Y	190	
C	I	G	A	A	A	F	S	X	Y	E	R	W	T	F	F	Q	A	Y		
TAC	TAC	TGC	TTC	ATC	ACC	CTC	ACC	ACC	ATC	GGC	TTC	GGC	GAC	TAC	GTG	GGC	CTG	CAG	627	
Y	Y	C	F	I	T	L	T	T	I	G	F	G	D	Y	V	A	L	Q	209	
Y	Y	C	F	I	T	L	T	T	I	G	F	G	D	Y	V	A	L	Q		
AAG	GAC	CAG	GCC	CTG	CAG	ACG	CAG	CCG	CAG	TAC	GTG	GCC	TTC	AGC	TTC	GTC	TAC	ATC	684	
K	D	Q	A	L	Q	T	Q	P	Q	Y	V	A	F	S	F	V	Y	I	228	
K	D	Q	A	L	Q	T	Q	P	Q	Y	V	A	F	S	F	V	Y	I		
CTT	ACG	GGC	CTC	ACG	GTC	ATC	GGC	GCC	TTC	CTC	AAC	CTC	GTG	GTG	CTG	CGC	TTC	ATG	741	
L	T	G	L	T	V	I	G	A	F	L	N	L	V	V	L	R	F	M	247	
L	T	G	L	T	V	I	G	A	F	L	N	L	V	V	L	R	F	M		

FIG. 8A

1201-CIP-DIV-2-00
 Fabrice Duprat, et al
 Family of Mammalian Potassium Channels, Their Cloning
 And Their Use, Especially for The Screening of Drugs

ACC ATG AAC GCC GAG GAC GAG AAG CGC GAC GCC GAG CAC CGC GCG CTG CTC ACG CGC	798
T M N A E D E K R D A E H R A L L T R	266
T M N A E D E K R D A E H R A L L T H	
AAC GGG CAG GCG GGC GGC GGA GGG GGT GGC AGC GCG CAC ACT ACG GAC ACC GCC	855
N G Q A G G G G G S A H T T D T A	285
N G Q A V G L G L S C L S G S L G D	
TCA TCC ACG GCG GCA GCG GGC GGC GGC TTC CGC AAC GTC TAC GCG GAG GTG CTG	912
S S T A A A G G G G F R N V Y A E V L	304
<u>VRPRD</u> PV TC AA A A G <u>GVGVGVGS</u> G F R N V Y A E V L	
CAC TTC CAG TCC ATG TGC TCG TGC CTG TGG TAC AAG AGC CGC GAG AAG CTG CAG TAC	969
H F Q S M C S C L W Y K S R E K L Q Y	323
H F Q S M C S C L W Y K S R E K L Q Y	
TCC ATC CCC ATG ATC ATC CCG CGG GAC CTC TCC ACG TCC GAC ACG TGC GTG GAG CAG	1026
S I P M I I P R D L S T S D T C V E Q	342
S I P M I I P R D L S T S D T C V E H	
AGC CAC TCG TCG CCG GGA GGG GGC GGC CGC TAC AGC GAC ACG CCC TCG CGA CGC TGC	1083
S H S S P G G G R Y S D T P S R R C	361
S H S S P G G G R Y S D T P S H P C	
CTG TGC AGC GGG GCG CCA CGC TCC GCC ATC AGC TCG GTG TCC ACG GGT CTG CAC AGC	1140
L C S G A P R S A I S S V S T G L H S	380
L C S G T Q R S A I S S V S T G L H S	
CTG TCC ACC TTC CGC GGC CTC ATG AAG CGC AGG AGC TCC GTG TGA ctggccccgagggacc 1200	
L S T F R G L M K R R S S V *	395
L A A F R G L M K R R S S V	
tggagcacctggggcgccggcggggacccctgtggaggccaggagactgccccctgtgccttctgcccagtg 1276	
ggaccccgacaacatccctcaccactctccccagcaccccatctccgactgtgcctgctgcaccagccggca 1352	
ggaggccggctctgaggacccctggggcccccattcgagccctgcaaattccgagaaatgtgaaacttgggtggg 1428	
tcagggagggaaaggcagaagctggagcctcccttccttggaaaatctaagaagctccagtcctcagagaccct 1504	
gctggtaccacacccacccatcgagggacttcatgttccgttacgtttgcatttatatacctctgtcct 1580	
gcttaggtctccacccatccctggttccaaagccagggtgtcatgtccaagtccatctactcagccccactcc 1656	
ccttcctcatcccaagctgtgtctcccaacccatccctcgatgtttgcattggcttgcagttatggagaaatgt 1732	
gaaacccagcagtcctaaagctggcccccagaaagcaggacagaaagaaggaggacaggcaggcaggaggg 1808	
gcgagctggaggcaggcaggcaggccctgtcagtctgcagaatggcactggaggtcaagcttaactggcctc 1884	
cagccacatttcatacgaggacttcagcctccagacactgcctttagaatctggAACAGACTTCAGA 1960	
ctcaccataattgtataattaccactctaaatttgcagtgatgtttgcctctgaaaactctatgtggc 2036	
caactgattcctttagtctcacaaaaaccctacttagtcatcaggcaggagttctcactcccatttacagatga 2112	
gaatactgaggcctggacaggtgaagtgaccagagcaaaaggcaaaagggtggggctgggtcagtggctcac 2188	
acctgtattcccaacactttggaggctgagggtggaggattgttgcaggcttgcagcccaggaaattcgagaccgc 2264	
acatagtgagacccatctctacaaaaaaaataaaaaaccctacttagtgcggcactggcctggagtcggc 2340	
cttggaggctgagggtggaggattgttgcggcactggcggcaggctgttagtgagccctgattgcaccactgt 2416	
ctccagcctgggtgacaggcagaccctgtctaaaaaaaaaaaaaaa 2465	

FIG. 8B

	1	-----MLOSLAGSSCVR-----LVERHRS---
	1	MAAPDILDPKSAAQNSKPRLSFSSKPTVLASRVESDSA
	1	-----MKR-----Q-NVR-----
		M1
TWIK-1	20	-----AWCFG-FLVLYIYLVLVFGAVVFSSSELPYEDLL
TREK-1	39	IINVMWKWKTIVSTIELVWVLYLIIGAAVFKALEQPQETSQ
TASK	8	-----TIALIVCTFTYLLVGAAVFDALESEPELIE
		P1
TWIK-1	53	RQELRKLRKFLEEHCELESEQQLEQELGRVLEASNYGV
TREK-1	77	RTTIVTIQKQTFIAQHACVNSTELDELQQIVAAINAGI
TASK	38	RQRLELRQQEERARYNLSQGG-YEELERVVRLKPHKA
		M2
TWIK-1	128	DGGKAFCIYYSVIGIPETLLEFLTAVVORITVHVTR--R
TREK-1	153	EGGKIFCIIYALLGIPLFGFLLAGVGDQIGTIFGKGIA
TASK	104	DGGKVFCCMEYALLGIPLTLVMEOSDGERINTEVRY--
		M3
TWIK-1	164	PVLYFHIRENGFSKQVVAIVHAVLILGFVTYSCFFPPIPAA
TREK-1	191	KVEDTFLIKWNVSQTKIRITISTIIFILFGCVLFVALPAV
TASK	139	LHRAKKGIGMRRADVSMANMVLIGFFSCISTLCIGAA
		P2
TWIK-1	202	VFSVLEDDDNFLESFYFCFISLSTIGLGDYVPGEGYNN
TREK-1	229	IFKHLEG-WSALDAIYFYVVIITLTIGFGDYVAG-GSD
TASK	177	AESHYEH-WTFEOAYYYCFITLTIGFGDYVABQKDQA
		M4
TWIK-1	239	QKERELYKIGITCYLLGLIAMLVLETECELHEKKF
TREK-1	264	I EYLDEYKPVVWEWILVGLAYFAAVLSMIGDWLRVISK
TASK	214	LOTQPOYVAESEFVYILTGLTVIGAFLNLVVLRFMTMNA
TWIK-1	277	RKMFYVKKDKD-----
TREK-1	302	KTKEEVGEFR-----
TASK	252	EDEKRDAEHRALLTRNGQAGGGGGSAHTTDTASSTA
TWIK-1	288	-----EDQVETIEHDQLSFSSITDQAAAGMK--
TREK-1	312	-----AHAAEWWTANVTAEFKETRRRLSVEI--
TASK	290	AAGGGGFRNVYAEVIEHQSMCSCLWYKSREKLQYSIPM
TWIK-1	313	---EDQKQNEPFVATQSSACVDGPANH-----
TREK-1	337	---YDKFQ RATSVKRKLSAELAGNNQELTPCMRTCL-
TASK	328	IIIPRDLSSTS DTCVEQSHSSPGGGGRYSDTPSRRCLCG
TWIK-1	337	-----
TREK-1	371	-----
TASK	366	APRSAISSVSTGLHSLSTFRGLMKRRSSV

FIG. 9A

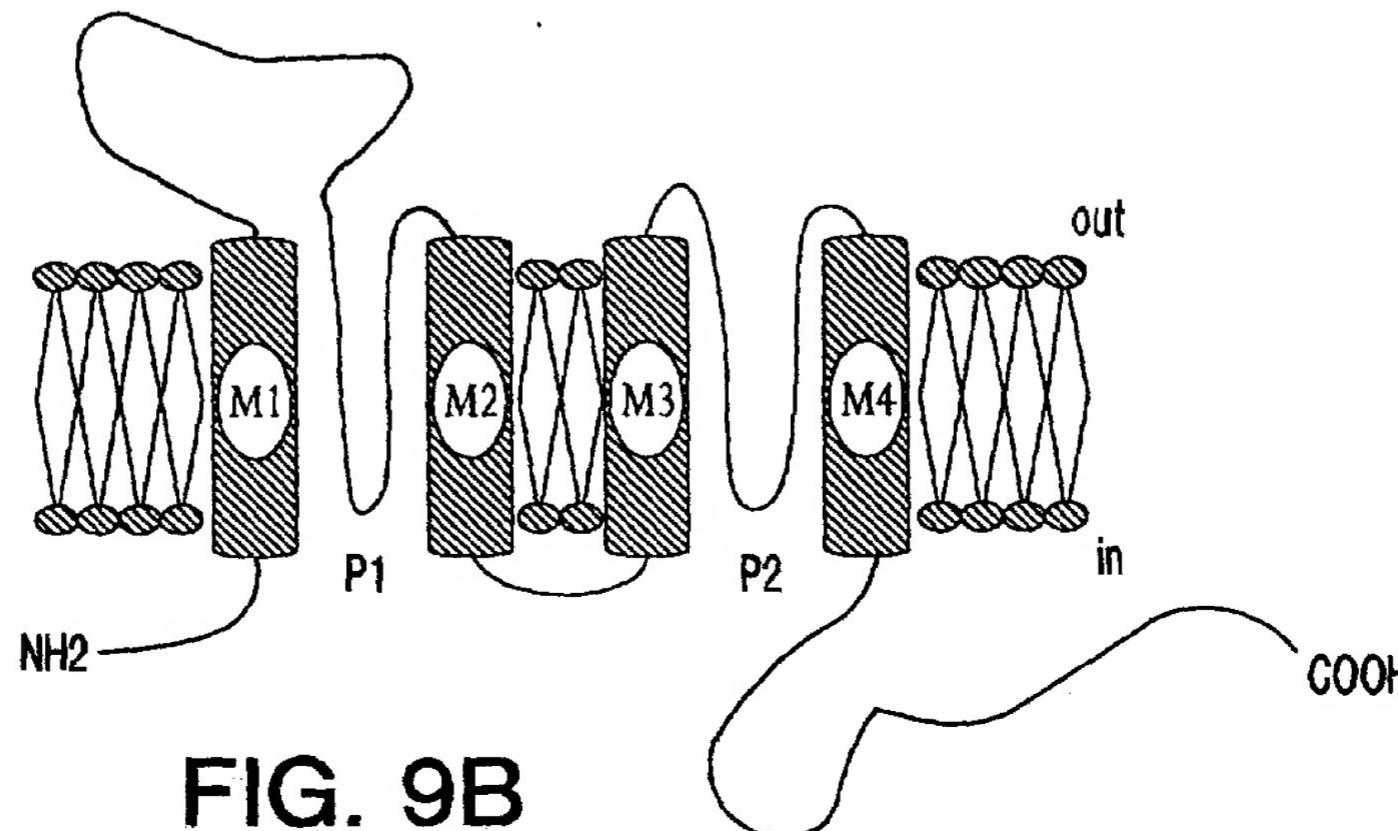


FIG. 9B

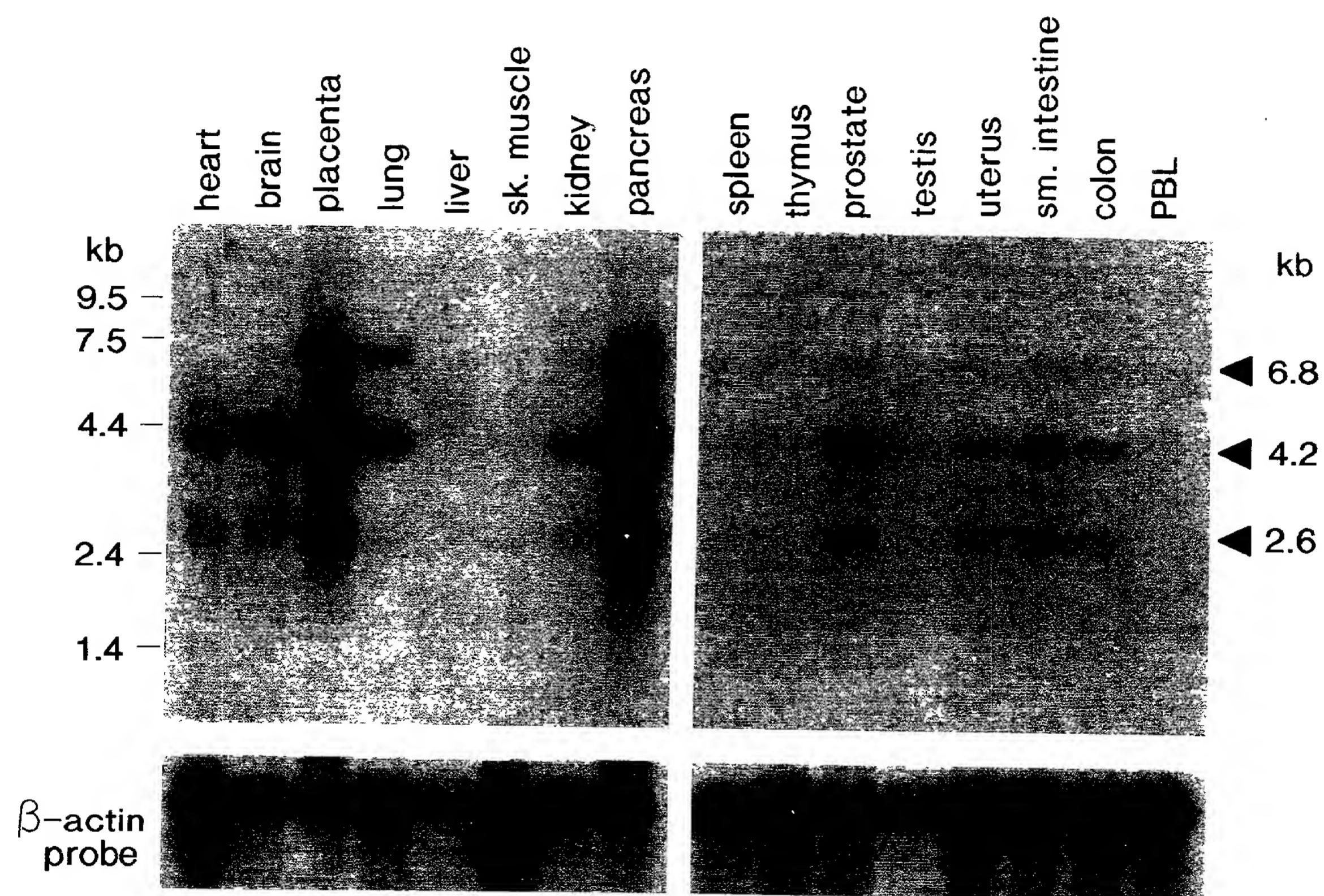


FIG. 10

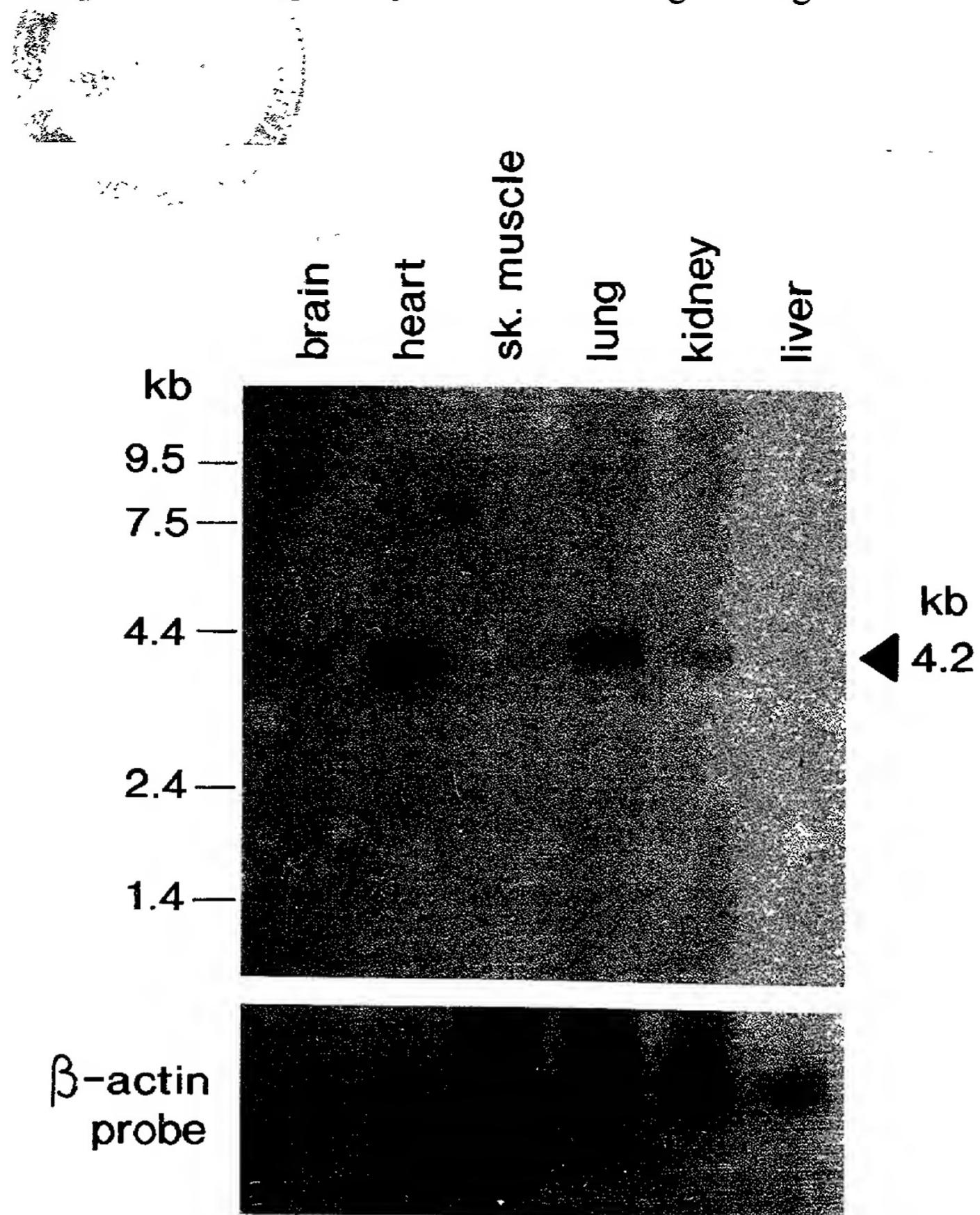


FIG. 11A

FIG. 11B

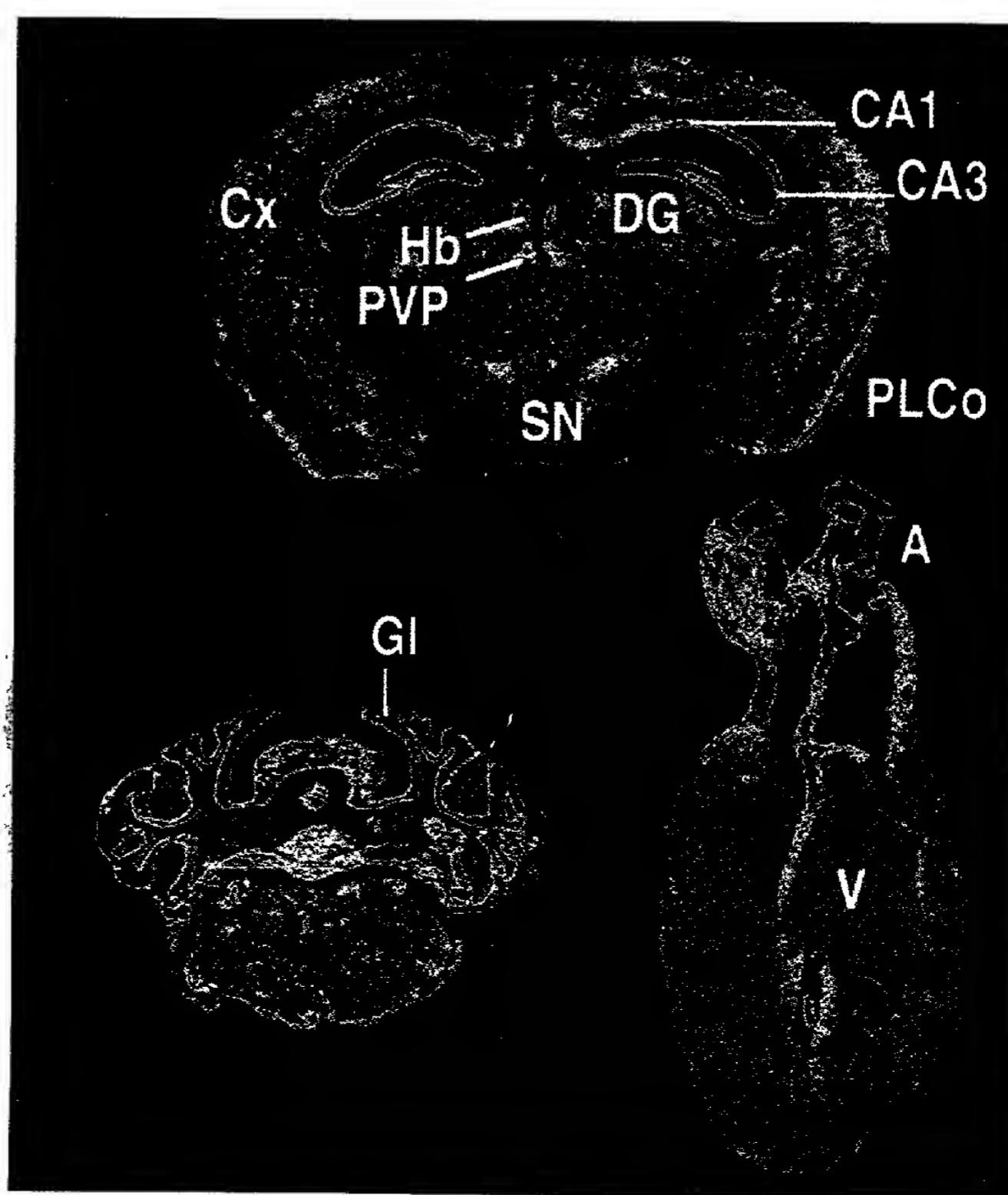


FIG. 11C

FIG. 11D

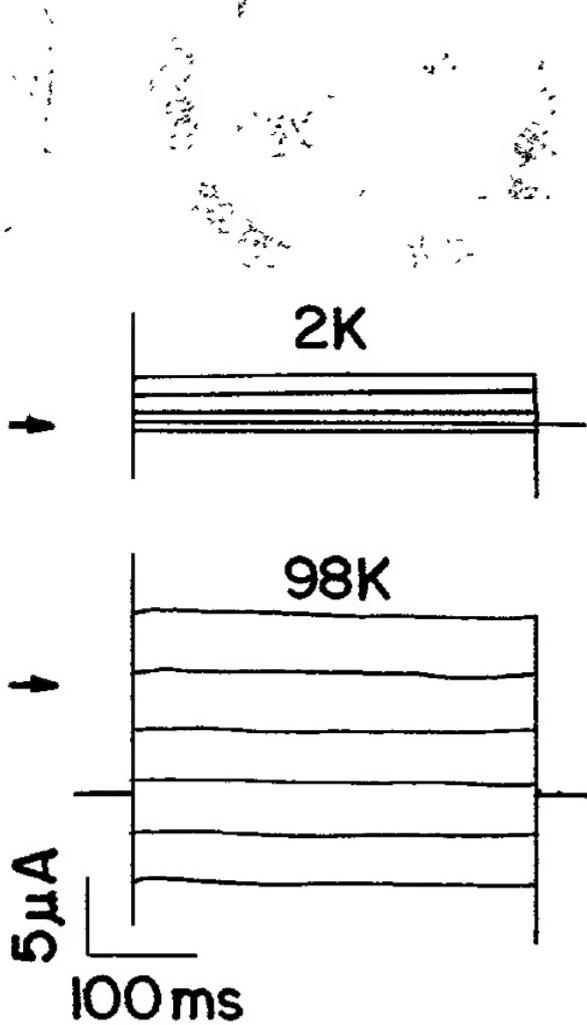


FIG. 12A

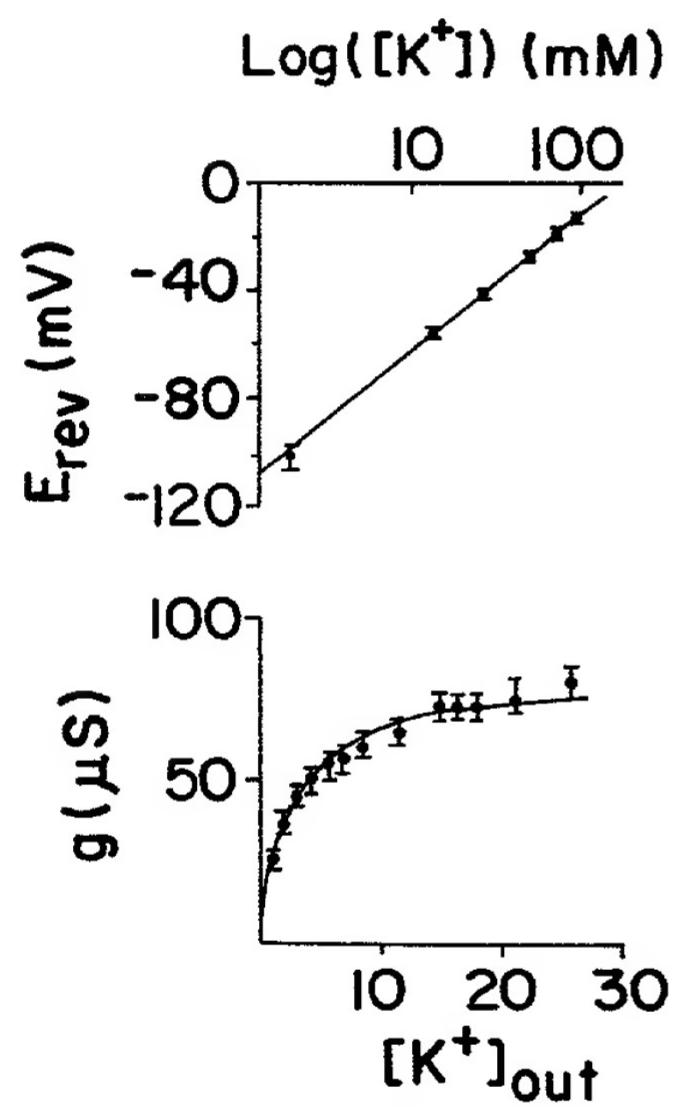


FIG. 12B

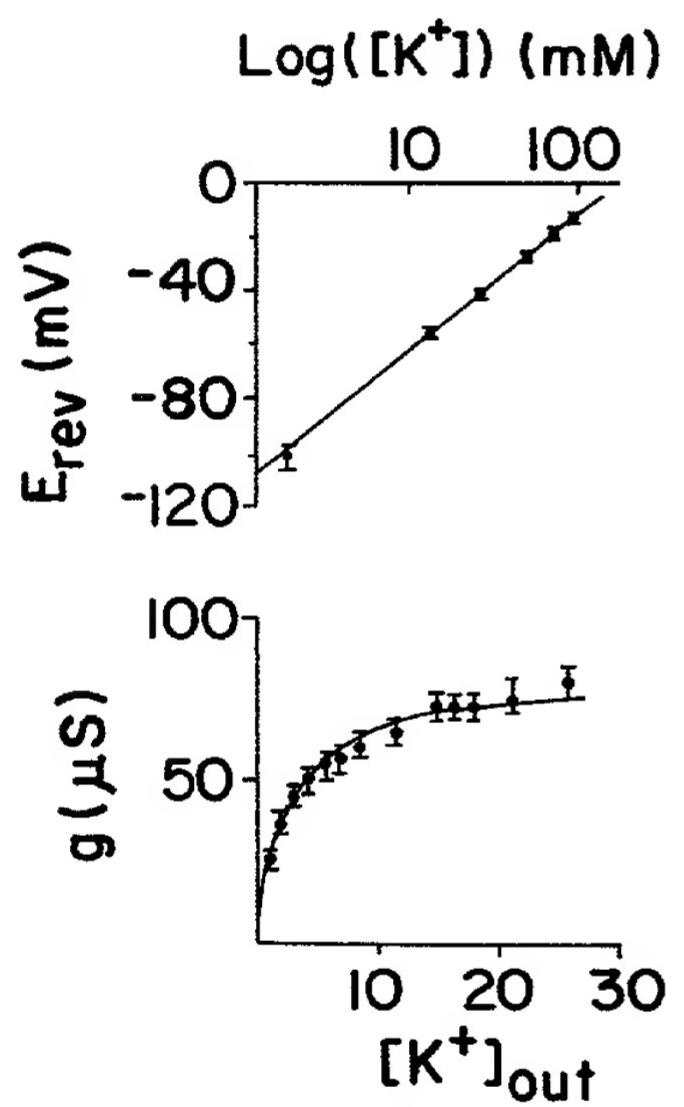


FIG. 12C

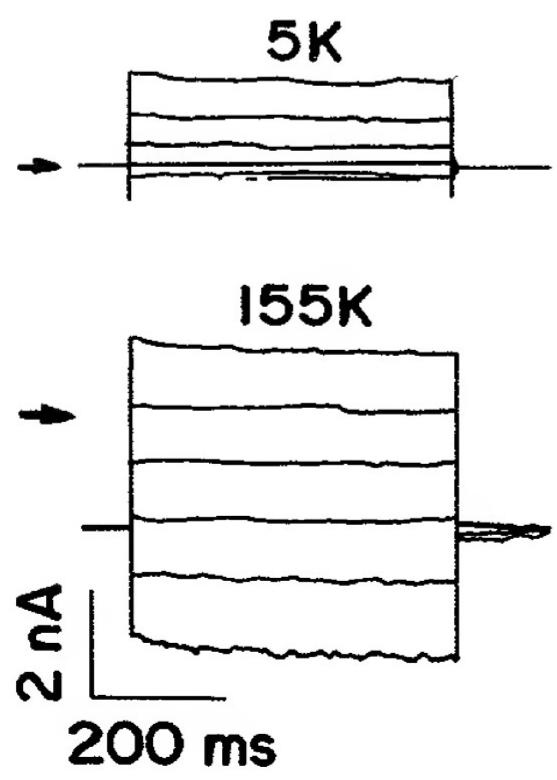


FIG. 12E

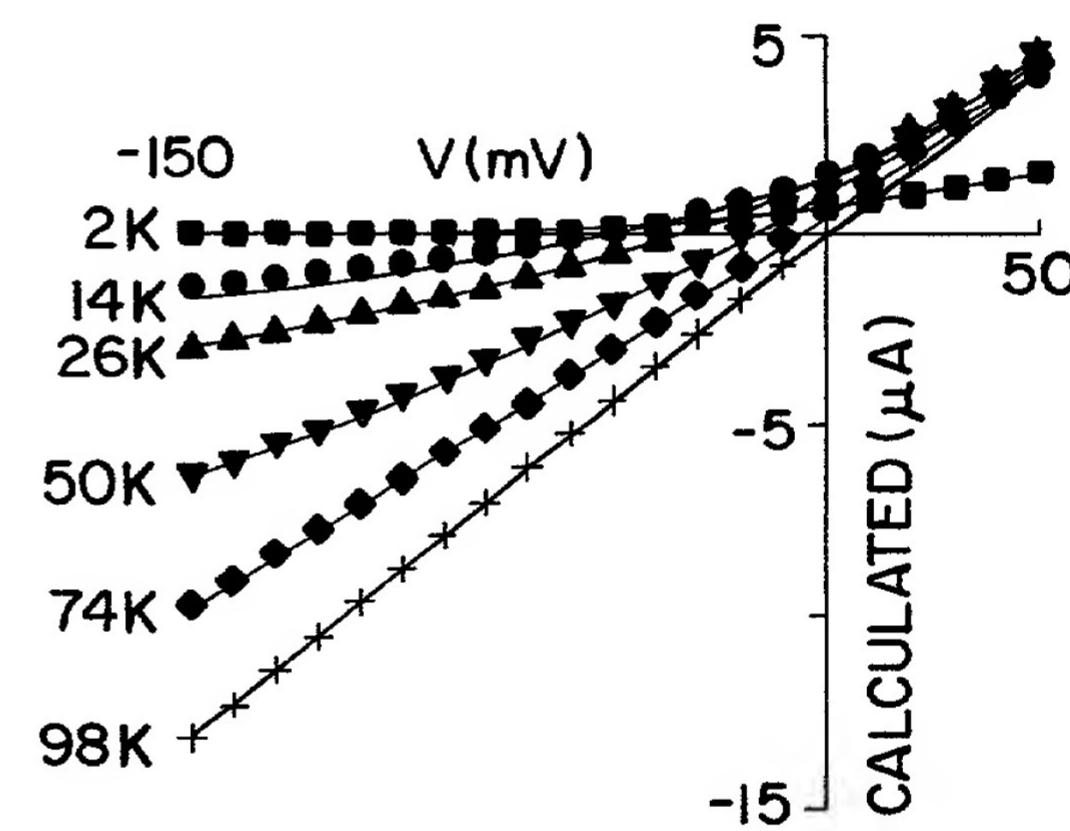


FIG. 12D

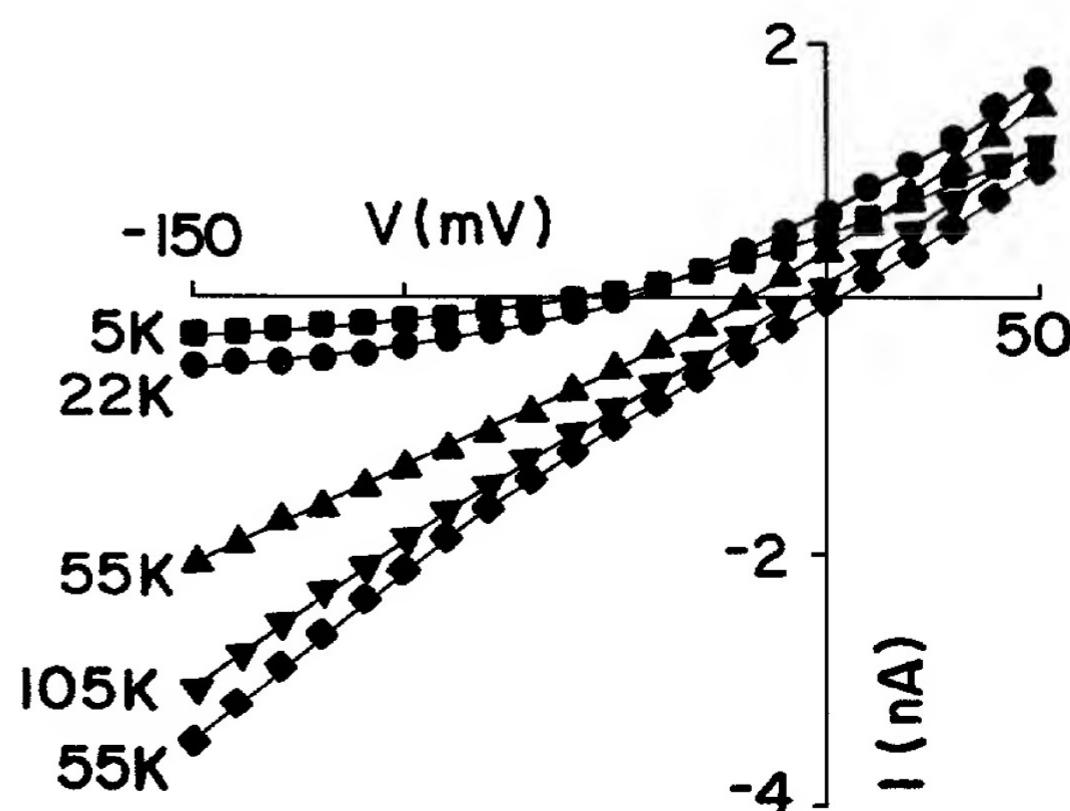


FIG. 12F

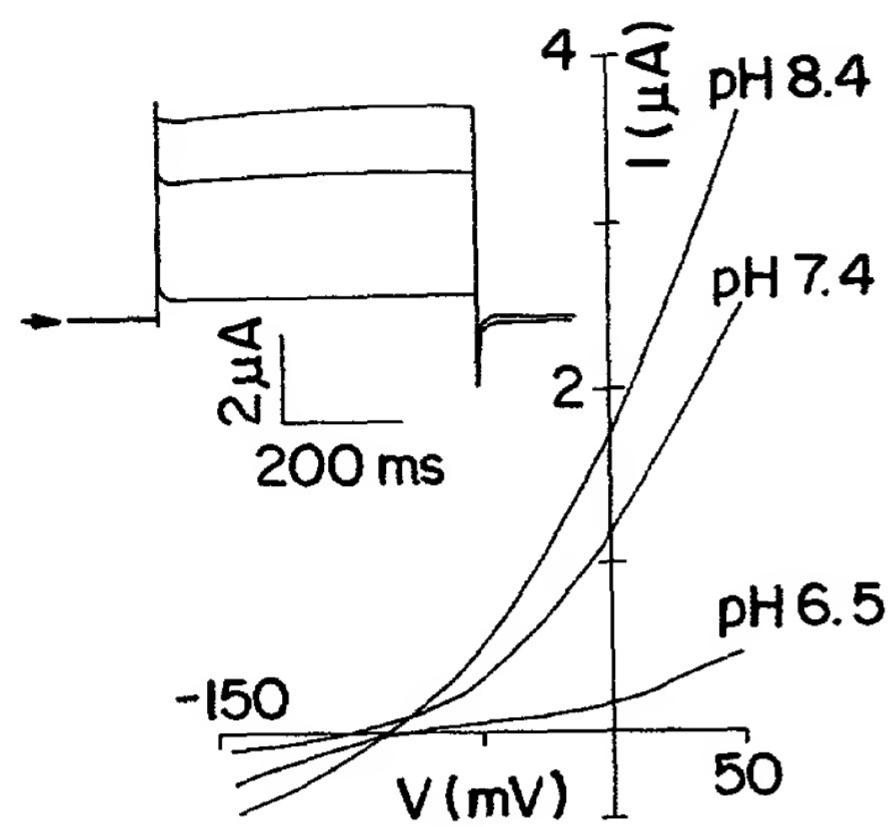


FIG. 13A

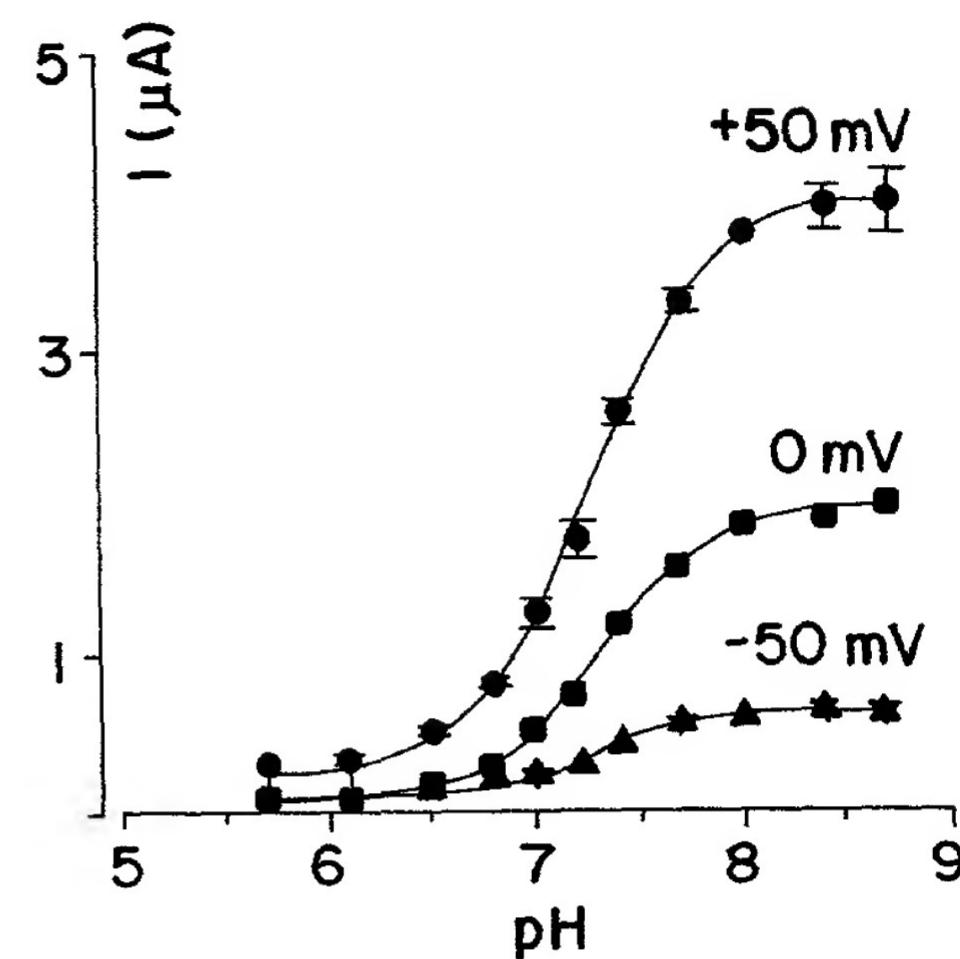


FIG. 13B

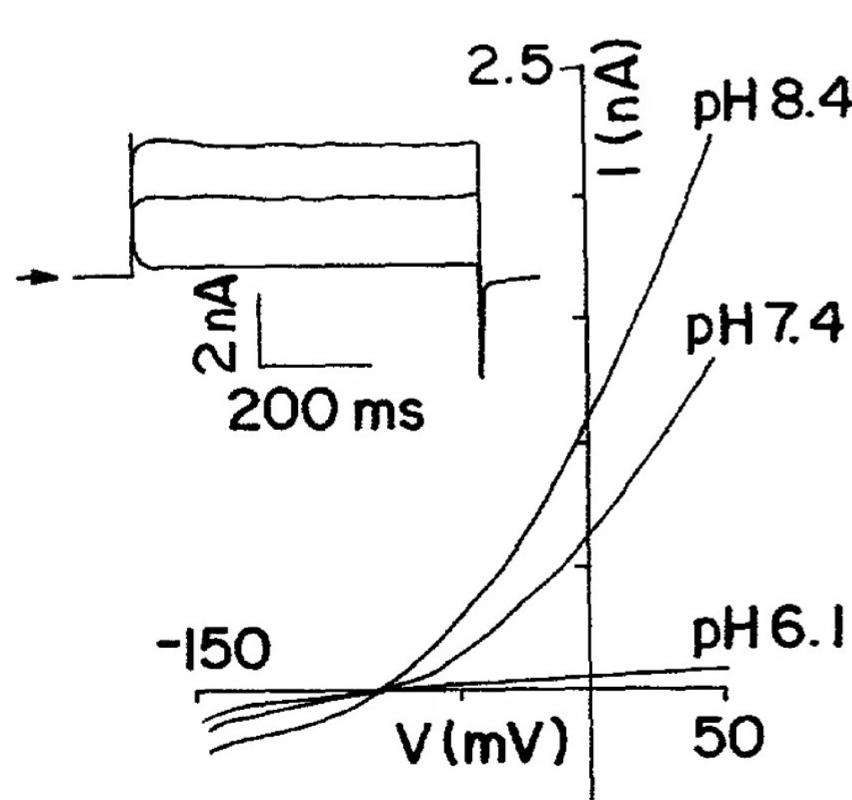


FIG. 13C

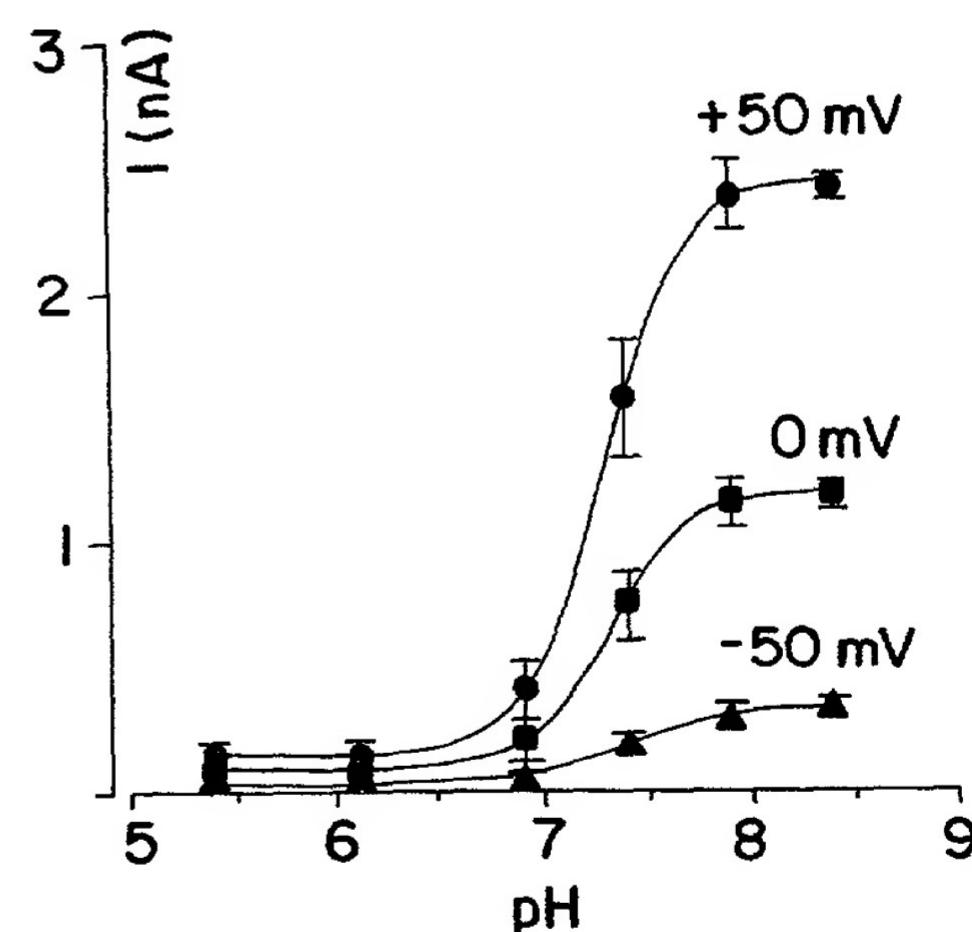


FIG. 13D